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From: McGarry, Sean
Sent: Monday, May 05, 2003 2:46 PM
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Subject: SEQ SEARCH

Sean McGarry 73484
AU 1635
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305-7028
09/917,963

Please, a length limited search of nucleotides 3050-3250 of SEQ ID NO:3 (nt≤100).

Thanks

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Searcher:_____
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Location:_____
Date Picked Up: 5/6

Searcher Prep/Review:
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:

Full text:
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____

Sequence Sys.:
WWW/Internet:
Other (specify):_____

McGarry, Sean

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Please, a length limited search of nucleotides 3050-3250 of SEQ ID NO:3 (nt≤100).

Thanks

GenCore version 5.1.4_p5_4578
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SM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:30:54 ; Search time 74 Seconds
(without alignments)
3375.455 Million cell updates/sec

Title: US-09-917-963-3_COPY_3050_3250
Perfect score: 201
Sequence: 1 ctaaaaqqaaaactaatqttt.....aacacaaacaaacaatttt 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621452466 residues

Total number of hits satisfying chosen parameters: 499754

Minimum DB seq length: 0
Maximum DB seq length: 100

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	33.8	16.8	93	10	US-09-960-352-13791	Sequence 13791, A
c 2	33.8	16.8	98	10	US-09-838-386-25	Sequence 25, Appl
c 3	33.6	16.7	27	9	US-09-937-279-162	Sequence 162, App
c 4	33.6	16.7	72	10	US-09-813-358-162	Sequence 162, App
c 5	33.2	16.5	55	10	US-09-920-300A-1151	Sequence 1151, Ap
c 6	33.2	16.5	55	12	US-10-033-528-1151	Sequence 1151, Ap
7	32.6	16.2	89	9	US-09-760-827-44	Sequence 44, Appl
c 8	32.4	16.1	72	10	US-09-919-580-443	Sequence 443, App
c 9	32.4	16.1	93	10	US-09-838-386-24	Sequence 24, Appl
10	32.2	16.0	89	10	US-09-925-301-774	Sequence 774, App
c 11	31.4	15.6	74	10	US-09-919-580-262	Sequence 262, App
12	31.4	15.6	83	9	US-10-102-806-495	Sequence 495, App
13	31.4	15.6	85	10	US-09-960-352-6425	Sequence 6425, Ap
c 14	31	15.4	73	10	US-09-919-580-542	Sequence 542, App
c 15	31	15.4	87	9	US-10-060-036-2822	Sequence 2822, Ap
16	31	15.4	93	9	US-09-925-299-497	Sequence 497, App
17	31	15.4	93	10	US-09-925-299-497	Sequence 497, App
c 18	31	15.4	100	10	US-09-815-343-385	Sequence 385, App
c 19	30.8	15.3	92	12	US-10-029-913-3	Sequence 3, Appli
20	30.6	15.2	86	9	US-09-[illegible]-7-49	[illegible]
21	30.6	15.2	86	10	US-09-960-352-1628	Sequence 1628, Ap
22	30.6	15.2	95	10	US-09-960-352-2344	Sequence 2344, Ap
c 23	30.4	15.1	72	10	US-09-[illegible]-89-221	Sequence 221, App
c 24	30.4	15.1	74	10	US-09-919-580-494	Sequence 494, App
25	30.4	15.1	75	10	US-09-963-[illegible]-223	Sequence 223, App
c 26	30.4	15.1	81	10	US-09-[illegible]-580-749	Sequence 749, App
27	30.4	15.1	90	9	US-10-[illegible]-572-572	Sequence 572, App
28	30.4	15.1	90	9	US-09-764-841-6711	Sequence 6711, Ap
c 29	30.4	15.1	100	10	US-09-270-696-908	Sequence 908, App
c 30	30.2	15.0	80	9	US-10-228-170-15	Sequence 15, Appl
31	30.2	15.0	80	10	US-09-961-106-25	Sequence 25, Appl
c 32	30.2	15.0	80	12	US-10-[illegible]-46-722-15	Sequence 15, Appl
c 33	30.2	15.0	82	10	US-09-919-580-220	Sequence 220, App
c 34	30.2	15.0	90	10	US-09-815-343-1277	Sequence 1277, Ap
c 35	30.2	15.0	100	10	US-09-919-580-428	Sequence 428, App
c 36	30	14.9	56	10	US-09-919-580-677	Sequence 677, App
37	30	14.9	64	10	US-09-983-965-42	Sequence 42, Appl
38	30	14.9	67	10	US-09-983-965-245	Sequence 245, App
39	30	14.9	67	10	US-09-983-965-455	Sequence 455, App
c 40	30	14.9	76	10	US-09-919-580-158	Sequence 158, App
c 41	30	14.9	77	9	US-10-val-585-282	Sequence 282, App
c 42	30	14.9	77	10	US-09-764-846-282	Sequence 282, App
43	30	14.9	77	10	US-09-960-352-8006	Sequence 8006, Ap
44	30	14.9	83	10	US-09-960-352-2095	Sequence 2095, Ap
45	30	14.9	95	10	US-09-960-352-8075	Sequence 8075, Ap

ALIGNMENTS

RESULT 1
US-09-960-352-13791/c
; Sequence 13791, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Muthalagan, Nanappan
; TITLE OF INVENTION: NUCLEIC ACID [illegible] FROM CHICKEN ANEMIA VIRUS AND USE THEREOF
; TITLE OF INVENTION: METHOD FOR [illegible]
; FILE REFERENCE: 1651.[illegible]
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13791
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (19)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone No. [illegible] 015-gl-K1 G4
US-09-960-352-13791

Query Match 16.8%; Score 33.8; DB 10; Length
Best Local Similarity 71.0%; Pred. No. 26;
Matches 44; Conservative 0; Mismatches 14; Indels

Qy 132 AAAACAAACACGTTGCTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAA 184
|||| ||||| | || || ||||||||||||||||
Db 73 AAAACAAAACAAATAATAAAAACAAC-AAAAAAAAAAAAAAAAAAAAA 21

Qy 192 AA 193
||
Db 19 AA 18

RESULT 2
US-09-838-386-25/c
; Sequence 25, Application US/09838386

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; Patent No. US20010055756A1
; GENERAL INFORMATION:
;  APPLICANT: Pellerin, Charles
;  APPLICANT:  Kukolj, George
;  TITLE OF INVENTION, Internal De No. US20010055756A1g Initiation Site of HCV NS5B
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: 1011.2180001
;  CURRENT APPLICATION NUMBER: US/09/838,786
;  CURRENT FILING DATE:  2001-04-20
;  PRIOR APPLICATION NUMBER: US 60/198,794
;  PRIOR FILING DATE: 2000-04-21
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Versio. 3.1
; SEQ ID NO 25
;   LENGTH: 98
;   TYPE: RNA
;   ORGAN SM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION, RNA initiation site
US-09-838-386-25

  Query Match             16.8%;  Score 33.8;  DB 10;  Length 98;
  Best Local Similarity   62.4%;  Pred. No. 26;
  Matches   54;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy     109 ACCAGTTCGTTAAGTATCACGCAAAACTAAACAGGTTCCCTAATCACCAAAAAAAAAAA 168
           |||| |     || | | | ||||| ||| |        || |  ||||||||||
Db      95 AGGAATATAAAAAAAAAAAAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 37

Qy     169 AAAAAAAAGTAAGACACAAACAAA 193
           |||||||| || | | |||||||
Db      36 AAAAAAAAAAAAAAAAAAAACAAA 13


RESULT 3
US-09-997-279-162/c
; Sequence 162, Application US/09997279
; Publication No. US20030059781A1
; GENERAL INFORMATION:
;  APPLICANT: Chonault, Patt A.
;  APPLICANT:  Xu, Jiangchun
;  TITLE OF INVENTION, COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION,  AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
;  FILE REFERENCE: 210121.501C1
;  CURRENT APPLICATION NUMBER: US/09/997,279
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 230
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 162
;   LENGTH: 77
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(77)
;   OTHER INFORMATION: n = A,T,C or G
US-09-997-279-162

  Query Match             16.7%;  Score 33.6;  DB 9;  Length 77;
  Best Local Similarity   64.0%;  Pred. No. 27;
  Matches   48;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy     118 TTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAA 177
           | ||  || |  |||| |  |     |||||||| |  ||||||||||||||  |||||
Db      77 TCAAAAATAAAAGGAACCCAGATTTNTTCCCTAAAAAAAAAAAAAAAAAAAANNAAAAA 18

Qy     178 GTAAGACACAAACAA 192
           || | | ||| ||
Db      17 AAAAAAAAAAAAAAA 3


RESULT 4
```

```
US-09-813-458-162/c
; Sequence 162, Application US/09813458
; Patent No. US20020048759A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Pyle, Ruth
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION, COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION,  AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER
;  FILE REFERENCE: 210121.501
;  CURRENT APPLICATION NUMBER: US/09/813,458
;  CURRENT FILING DATE:  2001-03-21
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 162
;   LENGTH: 77
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(77)
;   OTHER INFORMATION: n = A,T,C or G
US-09-813-458-162

  Query Match             16.7%;  Score 33.6;  DB 10;  Length 77;
  Best Local Similarity   64.0%;  Pred. No. 27;
  Matches   48;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy     118 TTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAA 177
           | ||  || |  |||| |  |     |||||||| |  ||||||||||||||  |||||
Db      77 TCAAAAATAAAAGGAACCCAGATTTNTTCCCTAAAAAAAAAAAAAAAAAAAANNAAAAA 18

Qy     178 GTAAGACACAAACAA 192
           || | | ||| ||
Db      17 AAAAAAAAAAAAAAA 3


RESULT 5
US-09-920-300A-1151/c
; Sequence 1151, Application US/09920300A
; Patent No. US20020126728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Seerist, Heather
;  TITLE OF INVENTION, COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE:  2001-07-41
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1151
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1151

  Query Match             16.5%;  Score 33.2;  DB 10;  Length 55;
  Best Local Similarity   75.9%;  Pred. No. 30;
  Matches   41;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy     140 ACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
           | || ||||| | ||  | ||||||||||||||||||  || | | ||| |||
Db      55 AAACGTTCCCAATCGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 6
US-10-033-528-1151/c
; Sequence 1151, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
```

; APPLICANT: Kinzl, Gordon E.
; APPLICANT: Meadner, Madeleine Joy
; APPLICANT: Xu, Jianzhun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1151
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1151

Query Match 16.5%; Score 33.2; DB 12; Length 95;
Best Local Similarity 75.9%; Pred. No. 30;
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 140 ACACGTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAAGTAAGACATAAACAAA 193
Db 65 AAACCTTCCCAATTCTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 7
US-09-768-827-44
; Sequence 44, Application US/09768827
; Patent No. US20020168648A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION
; TITLE OF INVENTION: ASSESSMENT, PREVENTION, AND THERAPY OF HUMAN
; TITLE OF INVENTION: PROSTATE CANCER
; FILE REFERENCE: MRI-007A
; CURRENT APPLICATION NUMBER: US/09/768,827
; CURRENT FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/178,525
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: US 60/183,245
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/190,139
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: US 60/208,126
; PRIOR FILING DATE: 2000-05-41
; PRIOR APPLICATION NUMBER: US 60/219,705
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 60/255,160
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-768-827-44

Query Match 16.2%; Score 32.6; DB 9; Length 89;
Best Local Similarity 64.3%; Pred. No. 49;
Matches 56; Conservative 9; Mismatches 29; Indels 0; Gaps 0;

Qy 111 GACTTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAA 170
Db 11 GAATTAATTAA[illegible] 89

Qy 171 AAAAAAGTAACACACAAA 189
Db 71 AAAAAAAAAAAAAAAAAA 89

RESULT 8
US-09-919-580-343/c
; Sequence 343, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jianzhun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERA-
; TITLE OF INVENTION: AND DIAGNOSIS [illegible] COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: [illegible]
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 343
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57, 58, 67
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-343

Query Match 16.1%; Score 32.4; DB 10; Length
Best Local Similarity 68.9%; Pred. No. 56;
Matches 42; Conservative 0; Mismatches 19; Indels

Qy 133 AAACCAAACACGTTCCCTAA[illegible] 193
Db 20 AAAAAAAATTCCNNGGG[illegible] 72

Qy 193 A 193
Db 10 A 10

RESULT 9
US-09-838-386-24/c
; Sequence 24, Application US/09838386
; Patent No. US20010055756A1
; GENERAL INFORMATION:
; APPLICANT: Pellerin, Charles
; APPLICANT: Kukolj, George
; TITLE OF INVENTION: Internal Le No. 5[illegible] Clon[illegible]A1, [illegible]
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1011.2180001
; CURRENT APPLICATION NUMBER: US/09/838,386
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 60/[illegible]
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 93
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: RNA initiation [illegible]
US-09-838-386-24

Query Match 16.1%; Score 32.4; DB 10; Length
Best Local Similarity 64.9%; Pred. No. 55;
Matches 48; Conservative 0; Mismatches 26; Indels

Qy 120 AAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAA 179
Db 74 AAGGAAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 133

Qy 180 AAGACACAAACAAA 193
Db 134 AAGACACAAACAAA 147

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Db      14 AAAAAAAAAAAAAA 1


RESULT 10
US-09-925-601-774
; Sequence 774, Application US/09925601
; Patent No. US20020052408A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,601
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 774
;  LENGTH: 89
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (20)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (74)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (76)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (77)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (79)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (83)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (86)
;  OTHER INFORMATION: n equals a,t,g, or c
US-09-925-601-774

  Query Match             15.0%;  Score 32.2;  DB 10;  Length 89;
  Best Local Similarity   64.8%;  Pred. No. 60;
  Matches   46;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     126 nACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACA 185
           || || || | ||   | | |    || | |||||||||||||||||| | || | |
Db       5 GAGGGAAACATCAGGNATGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 64

Qy     186 CAAACAAACCA 196
           ||| ||| | |
Db      65 AAAAAAAAANA 75


RESULT 11
US-09-919-580-262/c
; Sequence 262, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
;  APPLICANT: Pyle, Ruth
;  APPLICANT:  Xu, Jianqchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.552
;  CURRENT APPLICATION NUMBER: US/09/919,580
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 934
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 262
;  LENGTH: 74
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-919-580-262

  Query Match             15.6%;  Score 31.4;  DB 10;  Length 74;
  Best Local Similarity   77.6%;  Pred. No. 88;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     145 TTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
           |||| || | ||||||||||||||||||||| || | | ||| |||
Db      66 TTCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 18


RESULT 12
US-10-102-806-395
; Sequence 395, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 395
;  LENGTH: 83
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (11)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (13)
;  OTHER INFORMATION: n equals a,t,g, or c
;  NAME/KEY: misc_feature
;  LOCATION: (83)
;  OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-395

  Query Match             15.6%;  Score 31.4;  DB 9;  Length 83;
  Best Local Similarity   65.7%;  Pred. No. 91;
  Matches   44;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy     127 ACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACAC 186
           || | ||||  ||| |        || | ||||||||||||||||||||  || | |
Db       9 ACNGNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 68

Qy     187 AAACAAA 193
           ||| |||
Db      69 AAAAAAA 75


RESULT 13
US-09-960-352-6425
; Sequence 6425, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Iao, Nenqbinq
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
```

```
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/47 21(19298)[illegible]
;  CURRENT APPLICATION NUMBER: US/09/960,[illegible]
;  CURRENT FILING DATE: 2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6425
;   LENGTH: 85
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 28 BOVMSI-022-Q1 E1 G7
US-09-960-352-6425

  Query Match             15.[illegible]%;  Score [illegible]1.4;  DB 10;  Length 85;
  Best Local Similarity   67.7%;  Pred. No. 92;
  Matches   44;  Conservative    [illegible];  Mismatches   21;  Indels    [illegible];  Gaps    [illegible];

Qy        132 AAAA[illegible]AAA[illegible]AAAAAAAAAAAAAAAAAAAA[illegible]AA[illegible]AAAA[illegible]A 191
Db         15 AAAAAAAAAAAAAAA[illegible]AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA[illegible] 7[illegible]

Qy        192 AA[illegible]A 196
Db         75 AAACA 7[illegible]


RESULT 14
US-09-919-580-542/c
; Sequence 542, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
;  APPLICANT: Pyle, Ruth
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.552
;  CURRENT APPLICATION NUMBER: US/09/919,580
;  CURRENT FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 5[illegible]4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 542
;   LENGTH: 7[illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 62, 64, 67
;   OTHER INFORMATION: n = A,T,C or G
US-09-919-580-542

  Query Match             15.4%;  Score 41;  DB 10;  Length 7[illegible];
  Best Local Similarity   74.[illegible]%;  Pred. No. 1.1e+02;
  Matches   [illegible]7;  Conservative    0;  Mismatches   13;  Indels    [illegible];  Gaps    [illegible];

Qy        144 [illegible]TAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAA[illegible]AAA 19[illegible]
Db         [illegible] [illegible]NN[illegible]NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1[illegible]


RESULT 15
US-10-060-036-2822/c
; Sequence 2822, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT: Kalos, Michael D.
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Persing, David H.
;  APPLICANT: Hepler, William T.
;  APPLICANT: Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/[illegible]
;  CURRENT FILING DATE: 2002-0[illegible]
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 2822
;   LENGTH: 87
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 72, 79
;   OTHER INFORMATION: n = A,T,[illegible]
US-10-060-036-2822

  Query Match             15.4%;  Score [illegible];  DB 9;  Length 8[illegible];
  Best Local Similarity   75.[illegible]%;  Pred. No. [illegible]e+02;
  Matches   [illegible]7;  Conservative    [illegible];  Mismatches   12;  Indels [illegible]

Qy        [illegible] [illegible]AAT[illegible]A[illegible]AAAAAAAAAAAAAAAAAAAAA[illegible]AA[illegible]A[illegible]AAA[illegible]AAA [illegible]
Db         83 TTCCNAAAA[illegible]NAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA [illegible]


Search completed: May 12, 2003, [illegible]
Job time : 75 secs
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GeneCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:26:28 ; Search time 42 Seconds
(without alignments)
1467.667 Million cell updates/sec

Title: US-09-917-963-3_COPY_3050_3250
Perfect score: 201
Sequence: 1 ctaaaagtaaactaatattt.....tacacaaacaaaaaaaaattttt 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441462 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882924

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/iss_na/PCTUS_COMB1.seq:*
3: /cgn2_6/ptodata/1/iss_na/PCTUS_COMB2.seq:*
4: /cgn2_6/ptodata/1/iss_na/PCTUS_COMB3.seq:*
5: /cgn2_6/ptodata/1/iss_na/PCTUS_COMB4.seq:*
6: /cgn2_6/ptodata/1/iss_na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	33	16.4	75	2	US-08-776-944-13	Sequence 13, Appl
2	30.2	15.0	80	1	US-07-920-281C-25	Sequence 25, Appl
3	30.2	15.0	80	4	US-08-166-277-25	Sequence 25, Appl
4	30.2	15.0	80	4	US-09-254-627-15	Sequence 15, Appl
5	30	14.9	84	1	US-08-426-443-5	Sequence 5, Appli
6	29.6	14.7	91	4	US-09-404-879A-201	Sequence 201, App
7	29.4	14.6	84	1	US-08-664-596B-3	Sequence 3, Appli
8	29.4	14.6	84	1	US-08-738-367-3	Sequence 3, Appli
c 9	29.4	14.6	90	1	US-08-677-944-1	Sequence 1, Appli
c 10	29.4	14.6	90	4	US-09-254-048A-1	Sequence 1, Appli
c 11	29.4	14.6	90	4	US-09-921-203-1	Sequence 1, Appli
12	29	14.4	69	1	US-08-702-344-7	Sequence 7, Appli
13	29	14.4	69	1	US-08-702-344-22	Sequence 22, Appl
c 14	29	14.4	90	1	US-08-677-944-2	Sequence 2, Appli
c 15	28.6	14.2	65	4	US-09-415-784-32	Sequence 32, Appl
c 16	28.6	14.2	65	4	US-09-415-785A-32	Sequence 32, Appl
c 17	28.6	14.2	65	4	US-08-944-465-32	Sequence 32, Appl
c 18	28.6	14.2	65	4	US-09-415-868-32	Sequence 32, Appl
c 19	28.6	14.2	65	4	US-09-415-900-32	Sequence 32, Appl
c 20	28.6	14.2	90	4	US-09-065-058-16	Sequence 16, Appl
c 21	28.6	14.2	100	4	US-08-991-789A-30	Sequence 30, Appl
c 22	28.6	14.2	100	4	US-09-062-451-30	Sequence 30, Appl
c 23	28.6	14.2	100	4	US-09-598-326-30	Sequence 30, Appl
c 24	28.4	14.1	94	4	US-09-404-879A-261	Sequence 261, App
25	28.4	14.1	98	1	US-08-088-658-42	Sequence 42, Appl
26	28.4	14.1	98	2	US-08-471-907A-42	Sequence 42, Appl
c 27	28.2	14.0	65	4	US-09-051-079-6	Sequence 6, Appli
28	28	13.9	54	2	US-08-771-548-4	Sequence 4, Appl
29	28	13.9	55	1	US-08-137-456A-41	Sequence 41, Appl
c 30	28	13.9	61	4	US-09-[illegible]-[illegible]-7	Sequence 7, Appl
31	27.8	13.8	55	4	US-09-[illegible]-[illegible]-11	Sequence 11, Appl
32	27.8	13.8	55	4	US-09-[illegible]-[illegible]-13	Sequence 13, Appl
33	27.8	13.8	55	4	US-09-[illegible]-[illegible]-11	Sequence 11, Appl
34	27.8	13.8	55	4	US-09-[illegible]-[illegible]-13	Sequence 13, Appl
c 35	27.8	13.8	81	4	US-09-[illegible]-426-57	Sequence 57, Appl
36	27.4	13.6	61	4	US-09-[illegible]-[illegible]-7	Sequence 7, Appl
c 37	27.2	13.5	70	2	US-08-[illegible]-[illegible]-12	Sequence 12, Appl
38	27.2	13.5	85	1	US-08-[illegible]-[illegible]-97	Sequence 97, Appl
39	27.2	13.5	85	1	US-08-[illegible]-[illegible]-97	Sequence 97, Appl
40	27	13.4	50	1	US-08-[illegible]-[illegible]-1	Sequence 1, Appl
c 41	27	13.4	57	4	US-09-[illegible]-[illegible]-59	Sequence 59, Appl
c 42	27	13.4	57	4	US-09-[illegible]-[illegible]-59	Sequence 59, Appl
43	27	13.4	60	4	US-09-[illegible]-[illegible]-8	Sequence 8, Appl
44	26.8	13.3	54	2	US-08-[illegible]-[illegible]-24	Sequence 24, Appl
c 45	26.8	13.3	60	1	US-08-[illegible]-[illegible]-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-776-944-13/c
; Sequence 13, Application US/08776944
; Patent No. 5925520
; GENERAL INFORMATION:
; APPLICANT: TULLY, GILLIAN
; APPLICANT: SULLIVAN, KEVIN
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,944
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9417211.
; FILING DATE: 25-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAWFORD, ARTHUR R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1198-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; ORGANELLE: Mitochondrion
US-08-776-944-13

Query Match 16.4%; Score 33; DB 2; Length 75;

Best Local Similarity 78.7%; Pred. No. 13;
Matches 42; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 137 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 196
Db 64 CAAGCAAGCACAGCAATCAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 2
US-07-920-281C-25
; Sequence 25, Application US/07920281C
; Patent No. 5739020
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; APPLICANT: Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; TITLE OF INVENTION: Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,281C
; FILING DATE: 13-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald F.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 928-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..80
; OTHER INFORMATION: /label= terminator
; OTHER INFORMATION: /note= "3' terminal sequence of cDNA expression
; OTHER INFORMATION: vector complementary to alphavirus genomic RNA"
US-07-920-281C-25

Query Match 15.0%; Score 30.2; DB 1; Length 80;
Best Local Similarity 65.7%; Pred. No. 57;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 132 AAAACCAAACACCTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACA 191
Db 14 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 73

Qy 192 AACCATT 198
Db 74 AACTAGT 80

RESULT 3
US-08-466-277-25
; Sequence 25, Application US/08466277
; Patent No. 6190666
; GENERAL INFORMATION:
; APPLICANT: Garoff, Henrik
; Liljestrom, Peter
; TITLE OF INVENTION: DNA Expression Systems Based on
; Alphaviruses
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,277
; FILING DATE: 06-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/920,281
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 928-103P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Semliki Forest Virus
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..80
; OTHER INFORMATION: /label= terminator
; /note= "3' terminal sequence of cDNA expression
; vector complementary to alphavirus genomic RNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-466-277-25

Query Match 15.0%; Score 30.2; DB 4; Length 80;
Best Local Similarity 65.7%; Pred. No. 57;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 132 AAAACCAAACACCTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACA 191
Db 14 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 73

Qy 192 AACCATT 198
Db 74 AACTAGT 80

RESULT 4
US-09-284-627-15/C

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; Sequence 15, Application US/09284627
; Patent No. 6361944
;   GENERAL INFORMATION:
;        APPLICANT: Mitsubishi Chemical Corporation
;        TITLE OF INVENTION: Molecule assaying genotype to
;                            phenotype and use thereof
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Mitsubishi Chemical Corporation
;             STREET: 5-2, Marunouchi 2-chome
;             CITY: Chiyoda-ku
;             STATE: Tokyo
;             COUNTRY: JAPAN
;             ZIP: 100
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/284,627
;             FILING DATE: 02-Jun-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: JP 1996274855
;             FILING DATE: 17.10.96
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 80
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: synthetic DNA
;        FEATURE:
;             OTHER INFORMATION: has a sequence partly
;             complementary to SEQ ID NO: 17
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-284-627-15

  Query Match             15.0%;  Score 30.2;  DB 4;  Length 80;
  Best Local Similarity   74.5%;  Pred. No. 52;
  Matches   38;  Conservative    0;  Mismatches   13;  Indels     3;  Gaps     0;

Qy      191 AAICAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAAGCAATTTT 245
            || |  ||||||||||||||||||||  || | | ||| ||| ||  |   |
Db       56 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 5
US-08-420-443-5/c
; Sequence 5, Application US/08420443
; Patent No. 5607834
;   GENERAL INFORMATION:
;   GENERAL INFORMATION:
;     APPLICANT:  C. Bruce Badwell
;     TITLE OF INVENTION:  NUCLEIC ACID PROBES
;     NUMBER OF SEQUENCES:  9
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson
;       STREET:  225 Franklin Street
;       CITY:  Boston
;       STATE:  Massachusetts
;       COUNTRY:  U.S.A.
;       ZIP:  02110-2804
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       COMPUTER:  IBM PS/2 Model 50Z or 55SX
;       OPERATING SYSTEM:  MS-DOS (Version 5.0)
;       SOFTWARE:  WordPerfect (Version 5.1)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/420,443
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/979,[illegible]
;       FILING DATE:  19921210
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Y. Rocky Tsao
;       REGISTRATION NUMBER:  34,053
;       REFERENCE/DOCKET NUMBER:  [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  [illegible]
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  83
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       OTHER INFORMATION:  N stands for a 6-carbon
;       OTHER INFORMATION:  molecular linker.  See Fig. 7
;       OTHER INFORMATION:  of the specification
US-08-420-443-5

  Query Match             14.9%;  Score [illegible];  DB 1;  Length 83;
  Best Local Similarity   70.9%;  Pred. No. 63;
  Matches   39;  Conservative    0;  Mismatches   16;  Indels [illegible]

Qy      145 TTCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 197
            || |  | ||  |||||||||||||||||| || ||  || | | |||||  |
Db       63 TTACCAACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11

RESULT 6
US-09-404-879A-201/c
; Sequence 201, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  King, Gordon E.
;  APPLICANT:  Algate, Paul A.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE DIAG
;  TITLE OF INVENTION:  DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE:  210121.46202
;  CURRENT APPLICATION NUMBER:  US/09/404,879A
;  CURRENT FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  393
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 201
;   LENGTH: 91
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-404-879A-201

  Query Match             14.7%;  Score [illegible];  DB 4;  Length
  Best Local Similarity   64.7%;  Pred. No. 78;
  Matches   44;  Conservative    0;  Mismatches   24;  Indels [illegible]

Qy      132 AAAACAAACAACTCCCTAAT A [illegible] 191
            |||| ||| |          || | [illegible]
Db       91 AAAAAAAAAAAAAAAAAAAAAA [illegible] 24

Qy      192 AACCATT 199
            || | | |
Db       41 AAGCTGT 24

RESULT 7
US-08-664-596B-3
; Sequence 3, Application US/08664596B
; Patent No. 5807703
;   GENERAL INFORMATION:
;     APPLICANT:  Jacobs, Kenneth
```

```
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaValle, Edward
;    APPLICANT:  Rucle, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Evans, Cheryl
;    APPLICANT:  Spaulding, Vikki
;    APPLICANT:  Bowman, Michael
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 Cambridgepark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC DOS/MS DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/664,596B
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-664-596B-3

  Query Match              14.6%;  Score 29.4;  DB 1;  Length 84;
  Best Local Similarity    60.0%;  Pred. No. 86;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      114 TTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAA 173
            || || |  |  |    |||| ||| |          || |  ||||||||||||||||
Db        2 TTTTTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 61

Qy      174 AAAAGTAAGACACAAACAAA 193
            |||| || | | ||| |||
Db       62 AAAAAAAAAAAAAAAAAAA 81


RESULT 8
US-08-738-367-3
; Sequence 3, Application US/08738367
; Patent No. 5827688
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaValle, Edward
;    APPLICANT:  Rucle, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 Cambridgepark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/738,367
;      FILING DATE:
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  84 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-738-367-3

  Query Match              14.6%;  Score 29.4;  DB 1;  Length 84;
  Best Local Similarity    60.0%;  Pred. No. 86;
  Matches   48;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy      114 TTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAA 173
            || || |  |  |    |||| ||| |          || |  ||||||||||||||||
Db        2 TTTTTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 61

Qy      174 AAAAGTAAGACACAAACAAA 193
            |||| || | | ||| |||
Db       62 AAAAAAAAAAAAAAAAAAA 81


RESULT 9
US-08-677-944-1/c
; Sequence 1, Application US/08677944
; Patent No. 5770408
;  GENERAL INFORMATION:
;    APPLICANT:  Sato, Yoshihiro
;    TITLE OF INVENTION:  THE METHOD FOR THE AMPLIFICATION OF A BASE
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/677,944
;      FILING DATE:  10-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 95177768
;      FILING DATE:  13-JUL-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kilyk, John, Jr.
;      REGISTRATION NUMBER:  30763
```

```
;       REFERENCE/DOCKET NUMBER:  7216.1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312 616-5600
;       TELEFAX:  312 616-5700
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  90 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  synthetic DNA (oligonucleotide)
US-08-677-944-1

  Query Match             14.6%;  Score 29.4;  DB 1;  Length 90;
  Best Local Similarity   66.7%;  Pred. No. 86;
  Matches   42;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      131 CAAAACCAAACACGTTCCCTAATACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 190
            | | | |   |||   ||  ||  | ||||||||||||||||||||  | | | | |
Db       89 GCAAGCTTGGCACTGGCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  30

Qy      191 AAA 193
            |||
Db       29 AAA 27


RESULT 10
US-09-254-048A-1
; Sequence 1, Application US/09254048A
; Patent No. 6291669
; GENERAL INFORMATION:
;  APPLICANT: Kwiatkowski, Marek
;  APPLICANT:  Landegren, Ulf
;  APPLICANT:  Nilsson, Mats
;  TITLE OF INVENTION: SOLID PHASE SYNTHESIS
;  FILE REFERENCE: 11989.006001
;  CURRENT APPLICATION NUMBER:  US/09/254,048A
;  CURRENT FILING DATE:  1999-07-19
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 90
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: circularization probe
US-09-254-048A-1

  Query Match             14.6%;  Score 29.4;  DB 4;  Length 90;
  Best Local Similarity   66.7%;  Pred. No. 86;
  Matches   42;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy      131 CAAAACCAAACACGTTCCCTAATACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 190
            | | | |   |||   ||  ||  | ||||||||||||||||||||  | | | | |
Db       89 GCAAGCTTGGCACTGGCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  30

Qy      191 AAA 193
            |||
Db       29 AAA 27


RESULT 11
US-09-921-203-1
; Sequence 1, Application US/09921203
; Patent No. 6429309
; GENERAL INFORMATION:
;  APPLICANT: Kwiatkowski, Marek
;  APPLICANT:  Landegren, Ulf
;  APPLICANT:  Nilsson, Mats
;  TITLE OF INVENTION: SOLID PHASE SYNTHESIS
;  FILE REFERENCE: 11989-006001
;  CURRENT APPLICATION NUMBER:  US/09/921,203
;  CURRENT FILING DATE:  2001-08-02
;  PRIOR APPLICATION NUMBER: 09/254,048
;  PRIOR FILING DATE: 1999-07-19
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 90
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: circularization probe
US-09-921-203-1

  Query Match             14.6%;  Score 29.4;  DB 4;  Length
  Best Local Similarity   66.7%;  Pred. No. 86;
  Matches   42;  Conservative    0;  Mismatches   21;  Indels

Qy      131 CAAAACCAAACACGTTCCCTAATACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 190
            | | | |   |||   ||  ||  | ||||||||||||||||||||  | | | | |
Db       89 GCAAGCTTGGCACTGGCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Qy      191 AAA 193
            |||
Db       29 AAA 27


RESULT 12
US-08-702-344-7
; Sequence 7, Application US/08702344
; Patent No. 5723315
;  GENERAL INFORMATION:
;     APPLICANT:  Jacobs, Kenneth
;     APPLICANT:  McCoy, John
;     APPLICANT:  LaVallie, Edward
;     APPLICANT:  Racie, Lisa
;     APPLICANT:  Merberg, David
;     APPLICANT:  Treacy, Maurice
;     APPLICANT:  Spaulding, Vikki
;     TITLE OF INVENTION:  SECRETED EPITOPINS AND POLYNUCLEOTI
;     TITLE OF INVENTION:  ENCODING THEM
;     NUMBER OF SEQUENCES:  37
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genetics Institute, Inc.
;       STREET:  87 CambridgePark Drive
;       CITY:  Cambridge
;       STATE:  Massachusetts
;       COUNTRY:  U.S.A.
;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Patentin Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/702,344
;       FILING DATE:
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Scott A.
;       REGISTRATION NUMBER:  32,724
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 498 8224
;       TELEFAX:  (617) 876-5851
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  69 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-702-344-7

  Query Match             14.4%;  Score 29;  DB 1;  Length 69;
  Best Local Similarity   66.1%;  Pred. No. 1e+02;
```

```
  Matches   41;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy     132 AAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACA 191
           |||| ||| |         || | ||||||||||||||||||||  | | | ||| |
Db       1 AAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 60

Qy     192 AA 193
           ||
Db      61 AA 62


RESULT 13
US-08-702-344-22
; Sequence 22, Application US/08702344
; Patent No. 5723315
;  GENERAL INFORMATION:
;    APPLICANT:  Jacobs, Kenneth
;    APPLICANT:  McCoy, John
;    APPLICANT:  LaVallie, Edward
;    APPLICANT:  Rucki, Lisa
;    APPLICANT:  Merberg, David
;    APPLICANT:  Treacy, Maurice
;    APPLICANT:  Spaulding, Vikki
;    TITLE OF INVENTION:  SECRETED PROTEINS AND POLYNUCLEOTIDES
;    TITLE OF INVENTION:  ENCODING THEM
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/702,344
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8224
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  69 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-702-344-22

  Query Match             14.4%;  Score 29;  DB 1;  Length 69;
  Best Local Similarity   66.1%;  Pred. No. 1e+02;
  Matches   41;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy     132 AAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACA 191
           |||| ||| |         || | ||||||||||||||||||||  | | | ||| |
Db       1 AAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 60

Qy     192 AA 193
           ||
Db      61 AA 62


RESULT 14
US-08-677-944-2/c
; Sequence 2, Application US/08677944
; Patent No. 5770408
;  GENERAL INFORMATION:
;    APPLICANT:  Sato, Yoshihiro
;    TITLE OF INVENTION:  THE METHOD FOR THE AMPLIFICATION OF A BASE
;    TITLE OF INVENTION:  SEQUENCE
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  Two Prudential Plaza, Suite 4900
;      CITY:  Chicago
;      STATE:  IL
;      COUNTRY:  US
;      ZIP:  60601-6780
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/677,944
;      FILING DATE:  10-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 95177768
;      FILING DATE:  13-JUL-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kilyk, John, Jr.
;      REGISTRATION NUMBER:  30763
;      REFERENCE/DOCKET NUMBER:  72161
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-616-5600
;      TELEFAX:  312-616-5700
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  90 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  synthetic DNA (oligonucleotide)
US-08-677-944-2

  Query Match             14.4%;  Score 29;  DB 1;  Length 90;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+02;
  Matches   35;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     149 CTAAICAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
           | | ||  ||||||||||||||||||||  || | | ||| |||
Db      79 CGACTCTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45


RESULT 15
US-09-415-784-32/c
; Sequence 32, Application US/09415784
; Patent No. 6391642
;  GENERAL INFORMATION:
;       APPLICANT: Dubensky Jr., Thomas W.
;                  Polo, John M.
;                  Belli, Barbara A.
;                  Schlesinger, Sondra
;                  Dryga, Sergey A.
;                  Preiss, Ilya
;       TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS BASED VECTORS
;                           WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
;                           SYNTHESIS
;       NUMBER OF SEQUENCES: 125
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Seed Intellectual Property Law Group PLLC
;            STREET: 701 Fifth Avenue, Suite 6400
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104-7092
```

```
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: Patentin Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/415,784
;               FILING DATE: 08-Oct-1999
;               CLASSIFICATION: Unknown
;          ATTORNEY/AGENT INFORMATION:
;               NAME: McMasters, David D.
;               REGISTRATION NUMBER: 33,963
;               REFERENCE/DOCKET NUMBER: 4415.47711.US00
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (206) 622-4900
;               TELEFAX: (206) 682-6031
;     INFORMATION FOR SEQ ID NO: 42:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 65 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-415,784-42

  Query Match              14.2%;  Score 28.6;  DB 4;  Length 65;
  Best Local Similarity    79.1%;  Pred. No. 1.4e-02;
  Matches   41;  Conservative    0;  Mismatches    9;  Indels    4;  Gaps    1;

Qy      15 AAAAAAAAAAAAAAAAAAAAGTAATACACAAACAAACATTTT 2
           ||||||||||||||||||||  || | | || ||| | |||
Db      50 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTTT 7


Search completed: May 12, 2003, 01:06:55
Job time : 43 secs
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SeqCore version 5.1.4_p5_452a

Nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:22:59 ; Search time 927 Seconds
(without alignments)
3331.927 Million cell updates/sec

Title: US-09-917-963-3_COPY_3050_3250
Perfect score: 201
Sequence: 1 ctaaaaaaaaactaatgttt.....gacacaaaaaaaaaaaatttt 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_estfun:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: qb_est1:*
10: qb_est2:*
11: qb_htc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_estunc:*
16: em_estom:*
17: qb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	19.9	100	1*	BI003554	BI003554 MR3-HN012
c 2	37.4	18.6	72	2	HSM003184	AI338708 Homo sapi
* 3	36.8	18.3	74	1*	BM514574	BM514574 ky05003.y
4	36.4	18.1	67	2	HSM003183	AI338707 Homo sapi
c 5	36.4	18.1	89	10	AW246833	AW246833 2822538.s
c 6	35.8	17.8	95	9	AI473208	AI473208 IL56h05.s
c 7	35.6	17.7	88	1*	BI4[illegible]	[illegible]
8	35.4	17.6	92	9	AU[illegible]	AU[illegible]
c 9	35.2	17.5	88	9	AI4[illegible]	AI[illegible]
10	35	17.4	92	9	AI[illegible]	AI[illegible]
c 11	34.8	17.3	68	9	AI[illegible]	AI[illegible]
c 12	34.8	17.3	98	12	BE[illegible]	BE[illegible]
13	34.8	17.3	100	12	BE[illegible]	BE[illegible] MA
c 14	34.6	17.2	97	9	AI[illegible]	AI[illegible]
15	34.4	17.1	87	9	AI[illegible]	AI[illegible]
c 16	34.4	17.1	95	9	AI[illegible]	AI[illegible]
17	34.4	17.1	95	1*	BM[illegible]	BM[illegible]
c 18	34.2	17.0	79	2	HSM[illegible]	AI[illegible]
19	34.2	17.0	83	9	AI[illegible]	AI[illegible]
20	34.2	17.0	88	12	BE[illegible]	BE[illegible]
21	34.2	17.0	96	9	AA[illegible]	AA[illegible]
c 22	34	16.9	96	14	N27[illegible]	N27[illegible]
c 23	33.8	16.8	75	9	AI[illegible]	AI[illegible]
24	33.8	16.8	82	9	AA[illegible]	AA[illegible]
c 25	33.6	16.7	64	12	BE[illegible]	BE[illegible]
c 26	33.6	16.7	79	9	AI[illegible]	AI[illegible]
c 27	33.6	16.7	89	9	AI[illegible]	AI[illegible]
28	33.6	16.7	99	1*	BI[illegible]	BI[illegible]
29	33.6	16.7	100	9	AA[illegible]	AA[illegible]
c 30	33.4	16.6	60	2	HSM[illegible]	AI[illegible]
c 31	33.4	16.6	77	12	BI[illegible]	BI[illegible]
c 32	33.4	16.6	79	12	BF[illegible]	BF[illegible]
33	33.4	16.6	92	9	AI[illegible]	AI[illegible]
c 34	33.4	16.6	97	9	AI[illegible]	AI[illegible]
35	33.4	16.6	100	9	AA[illegible]	AA[illegible]
36	33.4	16.6	100	1*	BI[illegible]	BI[illegible]
c 37	33.2	16.5	65	1*	BI[illegible]	BI[illegible]
c 38	33.2	16.5	79	9	AU[illegible]	AU[illegible]
c 39	33.2	16.5	79	12	BI[illegible]	BI[illegible]
40	33.2	16.5	80	12	BG[illegible]	BG[illegible]
41	33.2	16.5	83	9	AA[illegible]	AA[illegible]
42	33.2	16.5	84	9	AI[illegible]	AI[illegible]
c 43	33.2	16.5	89	9	AI[illegible]	AI[illegible]
c 44	33.2	16.5	91	10	AW4[illegible]	AW4[illegible]
c 45	33.2	16.5	92	1*	BI[illegible]	BI[illegible]

ALIGNMENTS

RESULT 1
BI003554
LOCUS BI003554 [illegible] bp mRNA linear [illegible]
DEFINITION MR3-HN012-090201-0[illegible] HN12r Homo sapiens cDNA [illegible]
ACCESSION BI003554
VERSION BI003554.1 GI:144[illegible]
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
REFERENCE 1 (bases 1 to 100)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Naqui,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Goldman,G.H., Carvalho A.F., Matsukuma,A., Baia,G., Brunstein,A., deOliveira,J.F., Pacher,P., Jockyo ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de S Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. [illegible] (7), 4491-44[illegible]
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente [illegible] 4 andar, 05[illegible]
Brazil
Tel: +55 11-2704922
Fax: +55 11-2707001

```
            Email: asimpson@ludwig.org.br
            This sequence was derived from the PARESI/CLIT Human Cancer Genome
            Project, this entry can be seen in the following URL
            (http://www.ludwig.org.br/cgi-bin/estpath/libpath.pl) Re-sequence PCR: 16-12-
            09026] 002 h04st2 2001 02 09.ab1 1)
            Seq primer: puc 18 forward
            High quality sequence stop: 72.
FEATURES             Location/Qualifiers
     source          1..160
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BN0122"
                     /dev_stage="Adult"
                     /note="Organ: head_normal; Vector: pucic; Site_1: SmaI;
                     Site_2: SmaI. A mini-library was made by cloning products
                     derived from  PRESTES PCR (U.S. Letters Patent application
                     No. 196,716    Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       62 a      24 c       6 g      9 t
ORIGIN

  Query Match             19.9%;  Score 40;  DB 13;  Length 160;
  Best Local Similarity   68.8%;  Pred. No. 1.2e+04;
  Matches   55;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     117 CTTAAGCAGGAGGGGAAAACAAACAGTTCCTAATCAGGAAAAAAAAAAAAAAAAAA 176
           ||| |||| || ||| | || ||    | |||| | |||||| |||||| |||| 
Db      9 CTTGCGCATCACCTGAACGCAAAATAACTTATTAATAAAAAAAAATAAAAAAAAAAA 68

Qy     177 AGTAAGACACAAACAAACCA 196
           | || ||| | |||||| |
Db      69 AAAAAAACAAACACAAACAA 88


RESULT 2
HSM003184/c
ID   HSM003184  standard; RNA; EST; 72 BP.
XX
AC   AL048708;
XX
SV   AL048708.1
XX
DT   12-MAR-1999 (Rel. 59, Created)
DT   12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE   Homo sapiens mRNA, [3] DEC.p***E.11*_s1  [1:m...] ***  [1:p***E.11*];
XX
KW   EST; expressed sequence tag.
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-72
RA   Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT   ;
RL   Submitted (12-MAR-1999) * ***E IMB, Zentrale Forschungsgruppen
RL   MIPS, Am Kloptorspitz 18a D-82152 Martinsried, GERMANY
XX
CC   Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC   sequencing consortium of the German Genome Project
CC   tl sequence also available
CC   This clone is available at the RZPD in Berlin
CC   Please contact the RZPD; Ressourcenzentrum, Heubnerweg 6, 14059
CC   Berlin Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH   Key             Location/qualifiers
FH
FT   source          1..72
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /clone="DFFCp***66F0446"
FT                   /clone_lib "***6 (synonym: hbrain). Vector pAMP1; host
FT                   XL1Blue, sites:NotI + SalI"
FT                   /dev_stage "total"
FT                   /tissue_type "kidney"
XX
SQ   Sequence 72 BP; 9 A, 8 C, 5 G, 50 T, 0 other;

  Query Match             18.6%;  Score 37.4;  DB 2;  Length 72;
  Best Local Similarity   74.6%;  Pred. No. 3.4e+04;
  Matches   47;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     130 GGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAGTAAGACACAAA 189
           |||||| |||| ||||   || | |  ||||||||||||||||||||| || | |||
Db      63 GCAAAATAAAACCCGTTCATTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

Qy     190 CAA 192
           |||
Db       3 AAA 1


RESULT 3
BM514574
ID   BM514574                 74 bp    mRNA    linear   EST 15-FEB-2002
DEFINITION  ky05l04.y1 Parastrongyloides trichosuri PA SLI 1000 vl Murphy
            Chiapelli McCarter Parastrongyloides trichosuri cDNA 5', mRNA
            sequence.
ACCESSION   BM514574
VERSION     BM514574.1  GI:18685717
KEYWORDS    EST.
SOURCE      Parastrongyloides trichosuri.
  ORGANISM  Parastrongyloides trichosuri
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloididae; Parastrongyloides.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Papo,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Billier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Isagareishvili,R.
            , Penke,I., Kennedy,S., Maguire,T., Beck,C., Underwood,K., Stoptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,P., Kohn,S.
            , Shin,F., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University, School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Nematodes provided by Dr. Warwick Grant of AgResearch, New Zealand
            (warwick.grant@agresearch.co.nz). The library was constructed by
            Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu
            and jmccarte@watson.wustl.edu) at Washington University, St. Louis.
            DNA Sequencing by: Washington University Genome Sequencing Center
            St. Louis
            Seq primer: SL1 primer.
FEATURES    Location/Qualifiers
     source          1..74
                     /organism="Parastrongyloides trichosuri"
                     /db_xref="taxon:131310"
                     /clone_lib="Parastrongyloides trichosuri PA SL1 TOPO v1
                     Murphy Chiapelli McCarter"
                     /dev_stage "Parasitic adults"
                     /lab_host="DH10B"
                     /note "Vector: pCR11 TOPO (Invitrogen); Site_1: EcoRI; The
                     library was constructed by Claire Murphy, Brandi Chiapelli
                     , and Dr. James McCarter at Washington University, St.
                     Louis. Oligo(dT)-SL1 PCR based library. Parastrongyloides
                     trichosuri parasitic adult cDNA PCR products of size >400
                     nucleotides containing SL1 on the 5' end and oligo(dT) on
```

the 3' end were non-directionally cloned into pCR II 1000(Invitrogen) following the lopo TA cloning protocol. Nematodes were provided by Dr. Warwick Grant of AgResearch, New Zealand (warwick.grant@agresearch.co.nz). Worms were harvested from Australian brush tailed possum (Trichosurl vulpecula) and washed thoroughly to remove host contamination. Note that despite this effort, host contamination of the library is possible."

BASE COUNT 46 a 4 c 8 g 16 t
ORIGIN

Query Match 18.4%; Score 46.8; DB 13; Length 74;
Best Local Similarity 78.6%; Pred. No. 4.1e-04;
Matches 44; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 133 AAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAA 188
DB 19 AAATCAGAAATGTTCTCTAATAAGAAAAAAAAAACAAAAAAAAAAAAAAGAAAAAA 74

RESULT 4
HSM000183
ID HSM000183 standard; RNA; EST; 67 BP.
XX
AC AL038707;
XX
SV AL038707.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12 MAR 1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo Sapiens mRNA; EST DKFZp566E0446_r1 (from clone DKFZp566E0446)
XX
KW EST; expressed sequence tag.
XX
OS Homo Sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-67
RA Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12 MAR-1999) to the EMBL/GenBank/DDBJ databases.
RL MIPS, Am Klopferspitz 18a D 82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC sequencing consortium of the German Genome Project
CC st sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/qualifiers
FH
FT source 1..67
FT /db_xref="taxon:9606"
FT /organism "Homo Sapiens"
FT /clone="DKFZp566E0446"
FT /clone_lib "566 (synonym: htkd2). Vector pAMP1, 5.0"
FT X1-2blue; sites NotI + SalI"
FT /dev_stage "fetal"
FT /tissue_type="kidney"
XX
SQ Sequence 67 BP; 49 A; 5 C; 4 G; 9 T; 0 other;

Query Match 18.1%; Score 46.4; DB 2; Length 67;
Best Local Similarity 74.2%; Pred. No. 5e-04;
Matches 46; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 133 CGAAAACAAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACAAAA 192
DB 6 CGAAAATAAAACACGTTCTCTAATAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 65

QY 190 CA 191
DB 66 AA 67

RESULT 5
AW246833/c
LOCUS AW246833 mRNA
DEFINITION 2822630.3prime NIH_MGC_? Homo sapiens cDNA clone
mRNA sequence.
ACCESSION AW246833
VERSION AW246833.1 GI:6589826
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominida
REFERENCE 1 (bases 1 to 89)
AUTHORS NIH-MGC http://mgc.nci.nih.gov.
TITLE National Institutes of Health, Mammalian Gene
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2822630.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement, NIH/Clontech cDNA Library Prepared
Hong/Rubin Laboratory cDNA Library Arrayed by: Lawrence
Consortium (LLNL) DNA Sequenced by: Berkeley MGC
project Clone distribution: MGC clone distribution
be found through the I.M.A.G. Consortium/LLNL at
www.bic.llnl.gov/bic/mgc/mgcmain.html Base Calling
Scores: PHRED from University of Washington Genome
Trimming: cross_match from University of Washington
PHRAP suite. Poly-T Identification: patMatch.pl by
Drosophila Genome Project, University of Washington
http://www.genome.washington.edu. Low Quality Sequence
contiguous PHRED high quality bases following Very
Low Quality Sequence: Trace file contained 89 bases
peaks following vector sequence. Polyadenylation:
presence of a XhoI site followed by a run of 24
at the beginning of the sequence, this cDNA insert
polyadenylated.
Plate: LLCM9 row: 9 column: 1
High quality sequence stop: 41.
FEATURES Location/Qualifiers
source 1..89
/organism "Homo Sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2822630"
/clone_lib "NIH_MGC_7"
/tissue_type "Small cell carcinoma"
/cell_line "MC38"
/lab_host "DH10B (gamma-resistant)"
/note="Vector: pCMV-SPORT6; Site
EcoRI; cDNA made by oligo-dT primed
cloned into EcoRI/XhoI sites using the
adaptor: GGCACGAG(T)24. Size-selected
insert size 1.8kb. Library constructed
the laboratory of Gerald M. Rubin (Berkeley
California, Berkeley) using ZAP-cDNA
(Stratagene) and Superscript II RT (Life
BASE COUNT 10 a 10 c 19 g 50 t
ORIGIN

Query Match 18.1%; Score 46.4; DB 10; Length
Best Local Similarity 64.0%; Pred. No. 4.1e-04;
Matches 55; Conservative 0; Mismatches 31; Indels

QY 108 TAGGACTTCCTCAAGCATCACCCCAAAAATAAAAAGTTCCTAATCAGTA
DB 89 TTGCACCACTGCACTCCAGCCTGGGCAACAAGAGCAAGACTCCATCTCAA

QY 159 AAAAAAAAAACTAAGCACACAAACAAA

```
          ||||||||| || | |||| |||
Db      29 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 4


RESULT 6
A1473208/c
LOCUS       A1473208                 95 bp    mRNA    linear   EST 03-MAR-1999
DEFINITION  th56h05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2122925 3',
            mRNA sequence.
ACCESSION   A1473208
VERSION     A1473208.1  GI:4320253
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 95)
  AUTHORS   NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael B.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 878  Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 67.
FEATURES             Location/Qualifiers
     source          1..95
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2122925"
                     /clone_lib="NCI_CGAP_Kid11"
                     /tissue_type="Normal Kidney"
                     /lab_host="DH10B"
                     /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: NotI; Site_2: EcoRI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322476-1323911, 1456067-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo. "
BASE COUNT       19 a      4 c      1 g     71 t
ORIGIN

  Query Match             17.8%;  Score 45.8;  DB 9;  Length 95;
  Best Local Similarity   73.0%;  Pred. No. 4.7e+04;
  Matches   46;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy     141 GAAAACCAAACAGGTTCCCTAATCAGCAAAAAAAAAAAAAAAAAAAGTAAGACACAAAAAAAA 196
           |||||  ||| |  ||   |||  ||| |||||||||||||||||||  || | | |||
Db      78 GAAAAATAAAAATTTTTTTAAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 19

Qy     197 AAA 199
           |||
Db      18 AAA 16


RESULT 7
BI493021/c
LOCUS       BI493021                 88 bp    mRNA    linear   EST 20-AUG-2001
DEFINITION  UI-H-BI2-ajd-d-07-0-UI.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
            IMAGE:2484925 3', mRNA sequence.
ACCESSION   BI493021
VERSION     BI493021.1  GI:15342365
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   Roberts,N.C., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
            and Morton,C.C.
  TITLE     Isolation of novel and known genes from a human fetal cochlear cDNA
            library using subtractive hybridization and differential screening
  JOURNAL   Genomics 23, 42-50 (1994)
  MEDLINE   95140111
COMMENT     Contact: Morton, C. C.
            Department of Pathology and Obstetrics, Gynecology and
            Reproductive Biology
            Brigham and Women's Hospital
            75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
            Tel: 617 732 7980
            Fax: 617 738 6996
            Email: cmorton@bics.bwh.harvard.edu
            DNA sequencing and analyses were performed by National Institutes
            of Health Intramural Sequencing Center (NISC; see
            http://www.nisc.nih.gov).
            This clone is available royalty-free through LLNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Plate: LLAM6183  row: H  column: 14
            Seq primer: T7 primer.
FEATURES             Location/Qualifiers
     source          1..88
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2484925"
                     /clone_lib="Morton Fetal Cochlea"
                     /tissue_type="cochlea"
                     /dev_stage="16-22 week fetus"
                     /lab_host="SOLR cells (kanamycin resistant)"
                     /note="Organ: ear, Vector: pBluescript SK-; Site_1: EcoRI;
                     Site_2: XhoI; Reference: Genomics 23: 42-50 (1994) Cloned
                     unidirectionally. Primer: Oligo dT. Fetal cochlea, normal.
                     47% of inserts >0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
                     XR Vector. Library constructed by N. Roberts, C. Morton.
                     -5' adaptor sequence: 5' GAATTCGGCACGAG 3'  3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT       4 a      7 c      5 g     72 t
ORIGIN

  Query Match             17.7%;  Score 45.6;  DB 13;  Length 88;
  Best Local Similarity   75.9%;  Pred. No. 5.4e+04;
  Matches   44;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     136 GCAAACACGTTCCCTAATCAGCAAAAAAAAAAAAAAAAAAAGTAAGACACAAAAAAAA 194
           || ||   |||||  ||  |  ||||||||||||||||||||| |||| | ||| |||
Db      86 GCGAAGGTGTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAGAAAAAAAAAAA 29


RESULT 8
AU176071
LOCUS       AU176071                 92 bp    mRNA    linear   EST 05-JUL-2001
DEFINITION  AU176071 Marsupenaeus japonicus adult Marsupenaeus japonicus cDNA
            clone PJV472 reverse, mRNA sequence.
ACCESSION   AU176071
VERSION     AU176071.1  GI:14622478
KEYWORDS    EST.
SOURCE      Marsupenaeus japonicus.
  ORGANISM  Marsupenaeus japonicus
            Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
            Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
            Penaeidae; Marsupenaeus.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Kajitamaboru,J., Hiromo,I., Aoki,T., Itami,T. and Takahashi,Y.
  TITLE     Gene expression in non-infected and viral infected hemocytes of
            kuruma prawn (Penaeus japonicus)
```

```
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Takashi Aoki
            Aquatic Biosciences
            Tokyo University of Fisheries
            Konan 4-5-7, Tokyo, Minato-ku 108-8477, Japan
            Tel: 81-3-5463-0689
            Fax: 81-3-5463-0690
            Email: aoki@tokyo-u-fish.ac.jp.
FEATURES             Location/Qualifiers
     source          1..92
                     /organism="Marsupenaeus japonicus"
                     /db_xref "taxon:27405"
                     /clone "PJV472"
                     /clone_lib "Marsupenaeus japonicus adult"
                     /cell_type="hemocytes"
                     /dev_stage="adult"
                     /note="Vector: lambda ZAP II"
BASE COUNT       71 a       4 c       7 g       9 t       1 others
ORIGIN

  Query Match             17.6%;  Score 35.4;  DB 9;  Length 92;
  Best Local Similarity   68.6%;  Pred. No. 5.5e-04;
  Matches   48;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy     124 AtCAGCGGAAAAAGCAAACACGTTCCCTAATCACGAAAAAAAAAAAAAAAAAAAAAAAAAA 183
           | || |  |||| | || || |    ||| | |||||||||||||:|||||  || |
Db       8 AACAACGTAAAAACCTAATACACTTATAACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 67

Qy     184 CACAAACAAA 193
           | ||| |||
Db      68 AAAAAAAAAA 77


RESULT 9
AI499104
LOCUS       AI499104                 88 bp    mRNA    linear   EST 12-MAY-1999
DEFINITION  tc64g05.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2175104 3'
            similar to contains Alu repetitive element;, mRNA sequence
ACCESSION   AI499104
VERSION     AI499104.1  GI:4499086
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Fatelecostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael F.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.[illegible].gov/image_consortium
            Insert Length: 1061  Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 55
            POLYA No.
FEATURES             Location/Qualifiers
     source          1..88
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2175104"
                     /clone_lib="NCI_CGAP_Ut2"
                     /tissue_type="moderately-differentiated endometrial
                     adenocarcinoma, 4 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT2;
                     Site_2: NotI; 5'-directional; 3'
                     Average insert size: 1.0 kb; Life Technologies
                     11539-012"
BASE COUNT       4 a       9 c       5 g       9 t
ORIGIN

  Query Match             17.5%;  Score 35.2;  DB 9;  Length 88;
  Best Local Similarity   71.9%;  Pred. No. 7.1e-04;
  Matches   46;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     130 CCAAAACAAAACAGTTCCCTAATCACGAAAAAAAAAAAAAAAAAAAAAAAAAA 183
           |||||| ||| | |||| | | | ||||||||||||||||||  |||||
Db      82 CCAAAAATAAAACCCTCCCTAATCACGAAAAAAAAAAAAAAAAAAAAAAAAAA 131

Qy     184 CAAA 187
           ||||
Db     132 AAAA 135


RESULT 10
AL661110
LOCUS       AL661110                 92 bp    mRNA    linear   EST 23-JUL-2001
DEFINITION  AL661110 XGC-neurula Silurana tropicalis cDNA clone
            mRNA sequence.
ACCESSION   AL661110
VERSION     AL661110.1  GI:17675560
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Buckle,E., Taylor,E., Ashurst,J.L., Zorn,A.M. and
  TITLE     Sanger Xenopus tropicalis EST project 2001 (I...
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Buckle E
            Sanger Centre
            Hinxton, Cambridgeshire, CB1 1RA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: INeu042a17.sp6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (X
            constructed by Aaron M. Zorn.
FEATURES             Location/Qualifiers
     source          1..92
                     /organism="Silurana tropicalis"
                     /db_xref="taxon:8364"
                     /clone="INeu042a17"
                     /clone_lib="XGC neurula"
                     /dev_stage="neurula"
                     /lab_host="Escherichia coli DH10B"
                     /note="Vector: pCS2+; Site_1: EcoRI; Sit
                     was oligo dT primed from mRNA of poly A+
                     EcoRI-NotI cut cDNA was then ligated int
                     EcoRI at the 5' end and NotI at the 3'
BASE COUNT       72 a       5 c       4 g       7 t
ORIGIN

  Query Match             17.4%;  Score 35;  DB 9;  Length 92;
  Best Local Similarity   63.9%;  Pred. No. 9.6e-04;
  Matches   52;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps

Qy     111 CACTTCCTTAAACAACAGCCCAAAACTAAACACCCCCCTAACCACACAAAAA 164
           || ||||   | | |   ||| |  | || ||  |  |||  |||| |||||
Db       1 CAACTCCCCCCCCCAAAAAAA-CC-A-------CCCCAAAAAAAAAAAAAA 44

Qy     171 AAAAAAACTAACACACAAAAAAA 193
           ||||||| || | | ||| ||
Db      45 AAAAAAAAAAAAAAAAAAAAAA 67
```

```
RESULT 11
AI784145/c
LOCUS       AI784145                68 bp    mRNA    linear   EST 01-JUL-1999
DEFINITION  tb88c05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2125736 3' similar to contains Alu repetitive element;, mRNA
            sequence.
ACCESSION   AI784145
VERSION     AI784145.1  GI:5325954
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 55.
FEATURES             Location/Qualifiers
     source          1..68
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2125736"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208 325895 Soares NB2HF pool 1:
                     145032-147335, 147720 148104, 148872 149255, 15002 -
                     150407, 151176 152327 Soares NB2HF8 9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776 306411, 326136 322823, 326136 ... Soares NbHFB
                     pool 1: 723720 726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT        8 a      1 c      4 g     55 t
ORIGIN

  Query Match              17.3%;  Score 34.8;  DB 9;  Length 68;
  Best Local Similarity    72.6%;  Pred. No. 8.3e-04;
  Matches   45;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy        132 AAAACAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACA 191
              ||||  ||||  | ||    |||   |   |||||||||||||||||||   || | | ||| |
Db         63 AAAATGAAACCCCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

Qy        192 AA 193
              ||
Db          3 AA 2


RESULT 12
BF641545/c
LOCUS       BF641545                98 bp    mRNA    linear   EST 19-DEC-2000
DEFINITION  NF062C10IN1F1081 Insect herbivory Medicago truncatula cDNA clone
            NF062C10IN 5', mRNA sequence.
ACCESSION   BF641545
VERSION     BF641545.1  GI:11905703
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 98)
  AUTHORS   Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
            ,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula insect herbivory library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Korth K
            Dept. of Plant Pathology
            University of Arkansas
            217 Plant Science Building, Fayetteville, AR 72701, USA
            Tel: 501 575 5191
            Fax: 501 575 7601
            Email: kkorth@comp.uark.edu
            Insert Length: 98   Std Error: 0.00
            Plate: 062  row: C  column: 10
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1..98
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF062C10IN"
                     /clone_lib="Insect herbivory"
                     /tissue_type="Local and systemic leaves"
                     /dev_stage="mature"
                     /note="Vector: Lambda Zap. Library was generated from fully
                     expanded M. truncatula leaves of plants fed upon by
                     Spodoptera exigua (beet armyworm) for 24 hours. Systemic
                     (undamaged leaves from injured plants) and wounded leaves
                     were harvested and pooled."
BASE COUNT       16 a      8 c     13 g     61 t
ORIGIN

  Query Match              17.3%;  Score 34.8;  DB 12;  Length 98;
  Best Local Similarity    72.6%;  Pred. No. 6.4e+04;
  Matches   45;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy        134 AACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
              || | |||  ||| || ||   |   ||||||||||||||||||||   || | | ||| |||
Db         77 AATCCAACTTCTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 18

Qy        194 CC 195
               |
Db         17 AC 16


RESULT 13
BE724073
LOCUS       BE724073               100 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  19876c MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE724073
VERSION     BE724073.1  GI:10125369
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
```

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and all primers with phred
v0.980904.e. Vector identified by cross_match with the default
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGAC
Plate: 107 row: A column: 8
Seq primer: ATTTAGGTGACACTATAG.

FEATURES Location/qualifiers
source 1..100
/organism "Bos taurus"
/db_xref "taxon:9913"
/clone "MARC 4B V"
/tissue_type "pooled"
/lab_host "DH10B"
/note "Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

BASE COUNT 44 a 30 c 9 g 17 t
ORIGIN

Query Match 17.3%; Score 34.8; DB 12; Length 100;
Best Local Similarity 72.6%; Pred. No. 6.3e+04;
Matches 45; Conservative 0; Mismatches 17; Indels 9; Gaps 0;

Qy 132 AAAAGTAAAGACACAAACAAA 152
|||||| || | | ||| |||
Db 20 AAAAATAAAGATTTATTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 79

Qy 153 AA 154
||
Db 80 AA 81

RESULT 11
AI628325/c
LOCUS AI628325 97 bp mRNA linear EST 14-DEC-1999
DEFINITION ts36101.y1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2229081 3',
mRNA sequence.
ACCESSION AI628325
VERSION AI628325.1 GI:4665125
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 97)
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael E.
Emmert Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/http/www.ncbi/image.html
Insert Length: 1928 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 84
POLYA No.

FEATURES Location/qualifiers
source 1..97
/organism "Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2229081"
/clone_lib "NCI_CGAP_Ut4"
/tissue_type "Serous papillary carcinoma
pooled tumors"
/lab_host "DH10B"
/note="Organ: ovary; Vector: pCMV SPORT6;
Site_2: NotI; Site_1: SalI; Unidirectionally
Average insert size 1.9 kb. Life Technologies
11542-016"

BASE COUNT 16 a 1 c 0 g 2 t
ORIGIN

Query Match 17.2%; Score 34.6; DB 9; Length
Best Local Similarity 64.2%; Pred. No. 1.8e+04;
Matches 52; Conservative 0; Mismatches 29; Indels

Qy 153 TTTCTTTAAAGACACAAACAAA 174
|||||| || | | ||| |||
Db 96 GTTCCTAAAAAAAATTTAAAAAA 117

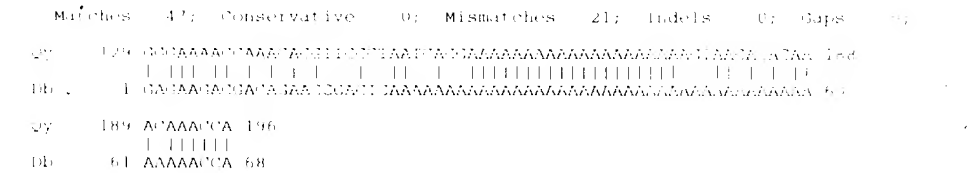
Qy 173 AAAAAGTAAGACACAAACAAA 193
||||| || | | ||| |||
Db 96 AAAAAAAAAAAAAAAAAAAAA 116

RESULT 15
AI349243
LOCUS AI349243 mRNA linear
DEFINITION ta74c12.x2 NCI_CGAP_Ut4 Homo sapiens cDNA clone
mRNA sequence.
ACCESSION AI349243
VERSION AI349243.1 GI:4086441
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
REFERENCE 1 (bases 1 to 87)
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap
TITLE National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Herbert M. [illegible], M.D., Michael E
M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome S
Clone distribution: NCI CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www.[illegible]/http/www/ncbi/image.html
Seq primer: -40UP from Gibco
FEATURES Location/qualifiers
source 1..87
/organism "Homo sapiens"
/db_xref "taxon:9606"
/clone="IMAGE:2049***"
/clone_lib "NCI_CGAP_BS2"
/tissue_type "Stomach, 34-73Mo"
/dev_stage "adult"
/lab_host "DH10B"
/note="Organ: bone marrow; Vector: pAMP1;
bone marrow, stomach, CD34+ cells, cDNA was
priming. Directionally cloned. Size sel
gel, average insert size 400 bp. Primary
non-amplified."

BASE COUNT 72 a 5 c 0 g 2 t
ORIGIN

Query Match 17.1%; Score 34.4; DB 9; Length
Best Local Similarity 69.1%; Pred. No. 2.6e+04;

Matches 47; Conservative 0; Mismatches 21; Indels 0; Gaps 0;



Search completed: May 12, 2003, 01:05:59
Job time : 981 secs

SeqCore version 5.1.4_p5_4573
Copyright (c) 1993 - 2003 Compugen Ltd.

QM nucleic - nucleic search, using sw model

Run on: May 11, 2003, 22:25:53 ; Search time 147 Seconds
(without alignments)
4079.263 Million cell updates/sec

Title: US-09-917-963-3_COPY_3050_3250
Perfect score: 201
Sequence: 1 ctaaqaqqaaactaqtqttt.....qacacaaacaaacqatttct 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185249 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: [illegible] *
2: [illegible] *
3: [illegible] *
4: [illegible] *
5: [illegible] *
6: [illegible] *
7: [illegible] *
8: [illegible] *
9: [illegible] *
10: [illegible] *
11: [illegible] *
12: [illegible] *
13: [illegible] *
14: [illegible] *
15: [illegible] *
16: [illegible] *
17: [illegible] *
18: [illegible] *
19: [illegible] *
20: [illegible] *
21: [illegible] *
22: [illegible] *
23: [illegible] *
24: [illegible] *

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
	1	34	16.9	71	24	AA164195	Labelled probe use
C	2	34	16.9	83	17	AA128139	Senescence-related
	3	33.8	16.8	81	21	AAC13249	Human secreted pro
C	4	33.6	16.7	77	22	AAS56538	Human cDNA for an
C	5	33.2	16.5	55	24	ABK45600	cDNA encoding solo
C	6	33	16.4	75	17	AAT17036	Human mitochondria
	7	32.6	16.2	89	22	AAS23322	Human prostate can
C	8	32.4	16.1	72	24	ABK54873	Human colon cancer
C	9	32.4	16.1	93	24	ABL41042	CDS #DNA SIR trans
	10	32.2	16.0	89	21	AA[illegible]	Hu
C	11	31.4	15.6	74	24	ABK547[illegible]	Hu
	12	31.4	15.6	83	21	AAE22[illegible]	Hu
C	13	31.4	15.6	98	12	AAQ11[illegible]	Ch
	14	31.2	15.5	51	22	AAL23[illegible]	Hu
C	15	31.2	15.5	84	22	AAL2[illegible]	Hu
C	16	31	15.4	73	24	ABK5[illegible]	Hu
	17	31	15.4	93	21	AAC[illegible]	Hu
C	18	31	15.4	100	23	AAS[illegible]	Hu
C	19	30.8	15.3	59	22	AAH[illegible]	Hu
	20	30.8	15.3	87	24	ABA[illegible]	Hu
C	21	30.8	15.3	92	18	AA1[illegible]	Hu
	22	30.6	15.2	86	22	AAS[illegible]	Hu
C	23	30.4	15.1	72	24	ABK54[illegible]	Hu
C	24	30.4	15.1	74	24	ABK54[illegible]	Hu
C	25	30.4	15.1	81	24	ABK55[illegible]	Hu
	26	30.4	15.1	90	22	ABA18[illegible]	Hu
	27	30.4	15.1	90	22	AAS40[illegible]	uN
	28	30.4	15.1	90	22	AAL04[illegible]	Hu
	29	30.4	15.1	90	22	AAK86[illegible]	Hu
C	30	30.4	15.1	90	24	ABL41[illegible]	Hu
C	31	30.2	15.0	80	19	AAV87[illegible]	Hu
C	32	30.2	15.0	82	24	ABK54[illegible]	Hu
	33	30.2	15.0	85	19	AAV32[illegible]	Hu
	34	30.2	15.0	85	22	AAE98[illegible]	Hu
C	35	30.2	15.0	90	23	AAS86[illegible]	Hu
C	36	30.2	15.0	100	24	ABK54[illegible]	Hu
C	37	30	14.9	56	24	ABK55[illegible]	Hu
C	38	30	14.9	76	24	ABK54[illegible]	Hu
C	39	30	14.9	77	22	AAS29[illegible]	Hu
	40	30	14.9	77	22	AAK98[illegible]	Hu
	41	30	14.9	77	22	AAK79[illegible]	Hu
	42	30	14.9	77	22	AAK84[illegible]	Hu
	43	29.8	14.8	62	22	AAD13[illegible]	Hu
	44	29.8	14.8	69	18	AA1880[illegible]	Hu
	45	29.8	14.8	69	18	AAV02[illegible]	Hu

ALIGNMENTS

RESULT 1
AA164195
ID AA164195 standard; DNA; 71 BP.
XX
AC AA164195;
XX
DT 19-JUN-2002 (first entry)
XX
DE Labelled probe used in a [illegible] protein/measurement
XX
KW [illegible] cancer; cytostatic; antipsoriatic; antiviral; anti-
KW arthritic; immunosuppressive; pesticide; fung[illegible]
KW herpes; alkylating; autoimmune disorder; psoriasis; scl[illegible]
KW rheumatoid arthritis; infection; anti-cancer agent; [illegible]
KW flavone; isoflavone; probe; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER - Oh,ppl.rylated"
FT misc_feature 22..71
FT /*tag= b
FT /note= "Can be cpl. hairy serially or[illegible]
FT 3' end"
XX
PN WO200180855-A1.
XX
PD 01-NOV-2001.
XX

```
PF   26-APR-2001; 2001WO-US11419.
XX
PR   27-APR-2000; 2000US-200172P.
XX
PA   (GERO ) GERON CORP.
XX
PI   Chin AC, Tolman RL, Gryaznov S, Matray T;
XX
DR   WPI; 2002-026116/03.
XX
PT   Use of substituted flavone or isoflavone compounds for inhibiting
PT   telomerase activity, and treating e.g. cancer -
XX
PS   Example 4; Page 92; 47pp; English.
XX
CC   The present sequence is that of a labelled probe used in a telomerase
CC   detection and measurement assay used to test the efficacy of the
CC   compounds of the invention as telomerase inhibitors. The specification
CC   describes a method of inhibiting telomerase activity in a cell,
CC   comprising contacting the cell with a flavone or isoflavone compound. The
CC   invention has cytostatic, antipsoriatic, antirheumatic, antiarthritic,
CC   immunosuppressive, protozoacide and fungicide activities. The compounds
CC   of the invention act as telomerase inhibitors and are used for treating
CC   telomerase mediated conditions or diseases, e.g. tumours. They may also
CC   be used to treat hyperproliferative or autoimmune disorders, such as
CC   psoriasis, rheumatoid arthritis; immune system disorders requiring immune
CC   system suppression; immune system reactions to poison ivy or poison oak;
CC   also nematode, protozoan and fungal infections. The compounds can be
CC   administered with other active agents, e.g. anti cancer agents. The
CC   compounds can also be administered to plants and soil infected with
CC   phytopathogenic organisms having telomerase activity, alone or in
CC   combination with other agents to control plant diseases. The compounds
CC   can be used for a wide variety of malignant cell types and are highly,
CC   selective, avoiding the problems of current cancer treatments, which are
CC   non specific and toxic.
XX
SQ   Sequence 71 BP; 56 A; 12 C; 0 G; 3 T; 0 other;

  Query Match             16.9%;  Score 34;  DB 24;  Length 71;
  Best Local Similarity   74.1%;  Pred. No. 1.8e-02;
  Matches   43;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     146 CCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 194
           || ||| |   |||||| |  |||||||||||||||||||| |  | | | ||| |||
Db       2 CCTAACCCTAACCCTAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 59


RESULT 2
AA128139/c
ID   AA128139 standard; DNA; 83 BP.
XX
AC   AA128139;
XX
DT   06-JAN-1997  (first entry)
XX
DE   Senescence-related gene sequence 10J1, 413.
XX
KW   Human; fibroblast; AIDS; enhanced differential display; mRNA preparation;
KW   senescent cell, quiescent cell, dividing cell, senescence related gene,
KW   gene expression; non-senescent cell, age related lipofuscin, retina, EDD,
KW   therapy; liver spot; donor tissue; senescent melanocyte; melanin;
KW   hypopigmentation; ss.
XX
OS   Synthetic.
XX
PN   WO9613610-A2.
XX
PD   09-MAY-1996.
XX
PF   24-AUG-1995;  95WO-US11230.
XX
PR   31-OCT-1994;  94US-332420.
XX
PA   (GERO-) GERON CORP.
XX
PI   Pera J, Funk W, Hirsch KS, Linskens MHK, Villeponteau B;
PI   West MD;
XX
DR   WPI; 1996-251464/25.
XX
PT   Identifying, isolating and regulating senescence-related genes -
PT   useful to ameliorate problems associated with accumulation of
PT   senescent cells, e.g. age-related lipofuscin accumulation in the
PT   retina and AIDS
XX
PS   Claim 8; Page 46; 135pp; English.
XX
CC   AA128076-128113, and AA128131-128173 represent novel senescent-related
CC   gene sequences isolated from fibroblasts using the method of the
CC   invention. In the method of the invention, mRNA is isolated from a
CC   senescent cell, and a young quiescent cell, and the mRNAs are amplified
CC   (using primers such as those shown in AA128044-128075) in separate
CC   reaction mixtures. The amplified sequences are then separated by size or
CC   charge, and the products are analysed to identify a gene from young
CC   quiescent cells and dividing cells, that is present at a different level
CC   from senescent cells. To enhance the method even more, it can be
CC   performed in conjuncture with an enhanced differential display (EDD)
CC   method (an mRNA preparation method) on the fibroblasts. The method can
CC   be used for the rapid and efficient identification and isolation of
CC   senescence-related genes and gene products, and to detect and distinguish
CC   between senescent and non-senescent cells. It can also be used to
CC   destroy cells expressing senescence specific (or related) gene products,
CC   and to screen for compounds capable of altering gene expression in
CC   senescent cells. The method can also be used to ameliorate problems
CC   associated with the accumulation of senescent cells such as age-related
CC   lipofuscin accumulation in the retina, and in the treatment of AIDS.
CC   Also, the method can be used to distinguish young cells from senescent
CC   cells in donor tissue, which is useful in removing senescent melanocytes
CC   overexpressing melanin which cause hypopigmentation, or liver spots.
XX
SQ   Sequence 83 BP; 20 A; 5 C; 10 G; 48 T; 0 other;

  Query Match             16.9%;  Score 34;  DB 17;  Length 83;
  Best Local Similarity   69.4%;  Pred. No. 1.8e-02;
  Matches   52;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy     100 GCTCTTGATAGGACTTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAA 159
           | |||  |||   || || |||    ||    |||  ||||   |||  | | |  ||
Db      82 GTTCTATATAGCCTTTGCTAAACAGCAACTAATAAATTAAACCTATTCTTCCAAAAAAAA 23

Qy     160 AAAAAAAAAAAAAAAAAGTAA 181
           |||||||||||||||||||  ||
Db      22 AAAAAAAAAAAAAAAAAAAAA 1


RESULT 3
AAC13249
ID   AAC13249 standard; cDNA; 81 BP.
XX
AC   AAC13249;
XX
DT   06-OCT-2000  (first entry)
XX
DE   Human secreted protein 5' EST, SEQ ID NO: 17324.
XX
KW   Human; 5' EST; expressed sequence tag, secreted protein, cDNA isolation;
KW   gene therapy, chromosome mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1033401-A2.
XX
PD   06-SEP-2000.
XX
PF   21-FEB-2000; 2000EP-0200610.
XX
```

```
DR   25-FEB-1999;  99US-0122487.
XX
PA   (GENSE ) GENSEL.
XX
PI   Dumas Milne Edwards J;  Duclert A;  Giordano J;
XX
DR   WPI; 2000-500081/45.
XX
PT   New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT   obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT   diagnostic, forensic, gene therapy and chromosome mapping procedures
XX
PS   Claim 1; SEQ ID 17424; 71pp; CD-ROM; English.
XX
CC   The present sequence is one of a large number of 5' ESTs derived from
CC   mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC   identified within the present sequence. The 5' ESTs were prepared from
CC   total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC   sequences usually correspond mainly to the 3' untranslated realm (UTR)
CC   of the mRNA because they are often obtained from oligo-dT primed cDNA
CC   libraries. Such ESTs are not well suited for isolating cDNA sequences
CC   derived from the 5' ends of mRNAs and even in those cases where longer
CC   cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC   5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC   used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC   in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC   They are used to obtain upstream regulatory sequences and to design
CC   expression and secretion vectors.
XX
SQ   Sequence 81 BP; 71 A; 2 C; 2 G; 6 T; 0 other;

  Query Match             16.8%;  Score 33.8;  DB 21;  Length 81;
  Best Local Similarity   72.1%;  Pred. No. 2e+02;
  Matches   44;  Conservative    9;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      138 AAATCAAACACATTTGCCIAATCAGGAAAAAAAAAAAAAAAAAAAAGTAACACACAAAACAA 192
            ||| ||| | ||| | ||  |  ||||||||||||||||||||  || | | ||| ||
Db        4 AAATAAAAGATGTTACAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 64

Qy      193 A 193
            |
Db       64 A 64


RESULT 4
AAS66548/c
ID   AAS66548 standard; cDNA; 77 BP.
XX
AC   AAS66548;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human cDNA for an ovarian cancer protein #162.
XX
KW   Human; ss; ovarian cancer protein; cancer; tumour; ovarian cancer;
KW   endometrial cancer; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200170976-A2.
XX
PD   27-SEP-2001.
XX
PF   20-MAR-2001; 2001WO-US009062.
XX
PR   21-MAR-2000; 2000US-190710P.
PR   22-JUN-2000; 2000US-214748P.
PR   19-DEC-2000; 2000US-257276P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J;  Pyle BA;  Stolk JA;
XX
DR   WPI; 2001-607531/69.
XX
PT   Nucleic acids encoding 222 polypeptides associated with
PT   endometrial cancers, useful for diagnosing, preventing and
PT   cancers -
XX
PS   Claim 1; Page 167; 187pp; English.
XX
CC   The invention relates to human polynucleotides encoding
CC   associated with ovarian and endometrial cancers. The poly
CC   the proteins they encode may be used in the prevention, d
CC   treatment of diseases associated with the inappropriate e
CC   ovarian and endometrial cancer polypeptides (OECPs). For
CC   polynucleotide (or an expression vector comprising the p
CC   and the OECP may be used to treat disorders associated wi
CC   expression by rectifying mutations or deletions in a pati
CC   that affect the activity of OECPs by expressing inactive
CC   supplement the patients own production of them. Additiona
CC   polynucleotide may be used to produce the OECPs, by inser
CC   acids into a host cell and culturing the cell to express
CC   polynucleotide and its complementary sequences may also b
CC   probes in diagnostic assays to detect and quantitate the
CC   similar nucleic acids in samples, and therefore which pat
CC   need of restorative therapy. The OECPs may also be used
CC   the production of anti-OECP antibodies and in assays for
CC   modulators of it's expression and activity. The anti-OECP
CC   antagonists may also be used to down regulate expression.
CC   The anti-OECP antibodies may also be used as diagnostics
CC   detecting the presence of OECP in samples (e.g. by ELISA
CC   immunosorbant assay (ELISA)) and to diagnose patients
CC   cancers. The present sequence is a ovarian and endometria
CC   cDNA of the invention.
XX
SQ   Sequence 77 BP; 9 A; 5 C; 7 G; 5 T; 0 other;

  Query Match             16.7%;  Score 33.6;  DB 22;  Length
  Best Local Similarity   64.0%;  Pred. No. 2.2e+02;
  Matches   32;  Conservative   27;  Mismatches   27;  Indels

Qy      118 TTAAGCATGACGGGAAAACCAAACACGTCTCTAATCAGAAAAAAAAAAAA 167
            | ||  || |  |||| |  |    |||| | |  | ||||||  ||
Db       72 TGAAAAATAAAAGGAACCCACATTTGTTTCTAAAAAAAAAAAAAAAAA 23

Qy      168 GTAAGACACAAACAA 192
            || | | ||| ||
Db       17 AAAAAAAAAAAAAAA 3


RESULT 5
ABK45600/c
ID   ABK45600 standard; cDNA; 5' BP.
XX
AC   ABK45600;
XX
DT   05-JUN-2002  (first entry)
XX
DE   cDNA encoding colon tumour protein SEQ ID No 1191.
XX
KW   Human; colon tumour; vaccine; colon cancer; immunotherapy;
KW   immunotherapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200212428-A2.
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US024218.
XX
PR   03-AUG-2000; 2000US-223284P.
PR   28-MAR-2001; 2001US-279763P.
PR   29-JUN-2001; 2001US-302051P.
XX
```

PA (CORI) CORIXA CORP.
XX
PI Kiyn GE, Mehtar M, Xu J, Secrist H;
XX
DR WPI; 2002-241739/29.
XX
PT New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT for diagnosing, preventing, and treating colon cancer, and as markers
PT for the progression of cancer
XX
PS Claim 1; SEQ ID No 1151; 147pp; English.
XX
CC The invention relates to polynucleotides encoding colon tumour proteins.
CC The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC compositions, such as vaccines, for the diagnosis, prevention, and
CC treatment of colon cancer. Polynucleotide sequences may be used as
CC hybridisation probes or primers, and in the design and preparation of
CC ribozyme molecules for inhibiting expression of tumour polypeptides and
CC proteins in tumour cells. The compositions are useful for stimulating an
CC immune response against cancer, particularly for the immunotherapy of
CC colon cancer, and as markers for the progression of cancer.
CC ABK41152 ABK46237 represent coding sequences of human colon tumour
CC proteins of the invention.
CC Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC for this patent did not form part of the printed specification but was
CC supplied by the European Patent Office.
XX
SQ Sequence 55 BP; 6 A; 2 C; 6 G; 41 T; 0 other;

Query Match 16.5%; Score 33.2; DB 24; Length 55;
Best Local Similarity 75.9%; Pred. No. 2.6e-02;
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 140 ACACGTTCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
||| || |||| | || | ||||||||||||||||||| || | | ||| |||
Db 55 AAACCTTCCCAATTCTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 6
AAI17036/c
ID AAI17036 standard; DNA; 75 BP.
XX
AC AAI17036;
XX
DT 04-OCT-1996 (first entry)
XX
DE Human mitochondrial DNA heavy chain primer H16190.
XX
KW Human; mitochondrial DNA; heavy chain; primer; polymorphism;
KW identification; discrete single nucleotide bases; method; screen;
KW genetic disease; DNA typing; forensic testing; microorganisms; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 1..42
FT /*tag= a
FT /note= "5' polyT tail, opt. polyA"
XX
PN WO9606187-A1.
XX
PD 29-FEB-1996.
XX
PF 21-AUG-1995; 95WO-GB01987.
XX
PR 25-AUG-1994; 94GB-0017211.
XX
PA (SULL) SOLICITOR AFFAIRS OF HM TREASURY.
XX
PI Sullivan K, Daly S;
XX
DR WPI; 1996-151490/15.
XX
PT Identifying single nucleotide bases adjacent to target sequence -
PT by annealing primer adjacent to the base and extension with
PT fluorescently labelled chain terminator, for simultaneous screening
PT of genetic diseases, or for forensic testing
XX
PS Claim 21; Page 24; 40pp; English.
XX
CC The present oligonucleotide is the human mitochondrial DNA heavy
CC chain primer AAH16190, where the No. is the position adjacent to the
CC polymorphism to which the primer end base binds. The primer is
CC used in a claimed method for the identification of at least 2
CC discrete, single nucleotide bases (nb), each adjacent to a target
CC sequence in a polynucleotide chain.
CC A sample is mixed with primers (P) that are complementary to the
CC characterised base sequence so that they anneal to the nb, at
CC least 2 types of chain terminator each having a characteristic
CC fluorescent label, and a chain extending enzyme so that the
CC terminators complementary to the nb are incorporated into P. The
CC extended P are then sepd. according to size or charge, and the
CC terminator incorporated identified. The method can be used to
CC screen for genetic diseases associated with single nb, and for DNA
CC typing, e.g. in forensic testing. It may also be used to screen
CC microorganisms.
XX
SQ Sequence 75 BP; 5 A; 4 C; 11 G; 54 T; 1 other;

Query Match 16.4%; Score 33; DB 17; Length 75;
Best Local Similarity 73.7%; Pred. No. 2.9e-02;
Matches 42; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 137 CAAACACGTTCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAACTAAGACACAAACAAA 193
||| || |||| | |||||| |||||||||||||||||||| || | | ||| |||
Db 64 CAAGCAAGTACAGCAATCAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 7
AAS23322
ID AAS23322 standard; cDNA; 89 BP.
XX
AC AAS23322;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human prostate cancer marker #44.
XX
KW Prostate cancer; human; cancer marker; metastasis; diagnostic;
KW therapeutic; immunogenic; ss.
XX
OS Homo sapiens.
XX
PN WO200154836-A2.
XX
PD 26-JUL-2001.
XX
PF 24 JAN 2001; 2001WO-US02318.
XX
PR 24 JAN 2000; 2000US-0178525.
PR 17 FEB 2000; 2000US-0183245.
PR 16-MAR-2000; 2000US-0190139.
PR 31-MAY-2000; 2000US-0208126.
PR 19 JUL 2000; 2000US-0219705.
PR 13-DEC 2000; 2000US-0255160.
XX
PA (MILL) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege W, Monahan JE;
XX
DR WPI; 2001-432912/46.
XX
PT Detecting and characterizing human prostate cancer comprises comparing
PT level of expression of marker in patient sample to normal level of
PT expression of marker in control non prostate cancer sample -
XX

PS Claim 1; Page 874; 975pp; English.
XX
CC The invention relates to a method of assessing whether a patient is
CC afflicted with prostate cancer (PCA) comprising comparing the level of
CC expression of a marker in a patient sample to the normal level of marker
CC expression in a control non-PCA sample, where a significant difference
CC between marker expression in the patient sample and the normal level is
CC an indication that the patient is afflicted with PCA. The method can also
CC be used for: (1) monitoring the progression of PCA in a patient; (2)
CC assessing the efficacy of a test compound for inhibiting PCA in a
CC patient; (3) assessing the efficacy of a therapy for inhibiting PCA in a
CC patient; (4) selecting a composition for inhibiting PCA in a patient;
CC (5) inhibiting PCA in a patient comprising administering the selected
CC composition; (6) making an isolated hybridoma which produces an antibody
CC useful for carrying out (1) comprising immunising a mammal using the
CC marker, isolating splenocytes from the mammal, fusing the splenocytes
CC with an immortalised cell line and screening individual hybridomas for
CC production of an antibody which specifically binds the marker; (7) an
CC antibody produced by the hybridoma of (6); (8) assessing the prostate
CC cell carcinogenic potential of a test compound; (9) inhibiting PCA in a
CC patient at risk for developing PCA; and (10) determining whether PCA has
CC metastasised in a patient or assessing the aggressiveness or incidence
CC of PCA. AAS23470-AAS23474 represent the amino sequences of prostate
CC cancer markers used in the method of the invention.
XX
SQ Sequence 89 BP; 66 A; 4 C; 8 G; 11 T; 0 other;

Query Match 16.2%; Score 32.6; DB 22; Length 89;
Best Local Similarity 64.3%; Pred. No. 3.5e-02;
Matches 50; Conservative 9; Mismatches 29; Indels 0; Gaps 0;

QY 111 GACTTCCTTAACACATGAGGGAAAACCAAACAACGTTCCTTAATTCAAAAAAAAAAAAAA 170
DB 11 GAATTAATTAACGCGCTCCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 70

QY 171 AAAAAAAGTAAGACACAAA 189
DB 71 AAAAAAAAAAAAAAAAAA 89

RESULT 8
ABK54873/c
ID ABK54873 standard; cDNA; 72 BP.
XX
AC ABK54873;
XX
DT 14-JUN-2002 (first entry)
XX
DE Human colon cancer associated cDNA, SEQ ID No 344.
XX
KW Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212280-A2.
XX
PD 14-FEB-2002.
XX
PF 6-JUL-2001; 2001WO-US23825.
XX
PR 04-AUG-2000; 2000US-223265P.
PR 02-OCT-2000; 2000US-237406P.
PR 27-MAR-2001; 2001US-279495P.
PR 03-JUL-2001; 2001US-302702P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Pyle PA, Xu J, Secrist H;
XX
DR WPI; 2002-257152/40.
XX
PT Novel polynucleotide encoding colon tumour polypeptides, useful as
PT vaccines for treating colon cancers.

XX
PS Claim 1; Page 247; 425pp; English.
XX
CC The invention relates to isolated [illegible] oligonucleotides (I) and
CC tumour polypeptides (II). (I) is useful for stimulating a
CC response in a patient and treating or for cancer in a pati
CC oligonucleotides derived from (I) are useful for detecting
CC of cancer in a patient. (I) and (II) are useful in pharma
CC compositions, e.g. vaccines, and other compositions for t
CC and treatment of colon cancer. A composition comprising a
CC selected from physiologically acceptable carriers and ex
CC and an antigen-presenting cell expressing (II) is useful
CC development of cancer in a patient. (I) is useful in the
CC preparation of ribozyme molecules for inhibiting express
CC polypeptides and (I). ABK54561-ABK54761 represent human
CC sequences of the invention.
XX
SQ Sequence 72 BP; 4 A; 7 C; 7 G; 11 T; 0 other;

Query Match 16.1%; Score 32.4; DB 24; Length
Best Local Similarity 68.9%; Pred. No. 5.8e-02;
Matches 42; Conservative 0; Mismatches 19; Indels

QY 133 AAACAAAACAACGTTCCTTAAT-TCAAAAAAAAAAAAAAAAAAAA 179
DB 70 AAANAAAATTCGCGCNCCCTTAAATTCAAAAAAAAAAAAAAAAAAAA 29

QY 193 A 193
DB 10 A 10

RESULT 9
ABL41042/c
ID ABL41042 standard; DNA; 93 BP.
XX
AC ABL41042;
XX
DT 12-AUG-2002 (first entry)
XX
DE GUS mRNA UTR fragment amplified [illegible] 8.
XX
KW Translation; untranslated region; UTR; pathogen; virus;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002095483-A.
XX
PD 02-APR-2002.
XX
PF 25-SEP-2000; 2000JP-0291084.
XX
PR 25-SEP-2000; 2000JP-0291084.
XX
PA (TOYE) TOYOJA JIDOSHA KK
PA (KONE) KONEN KLEB CORP.
XX
DR WPI; 2002-439991/47.
XX
PT Screening potential translational control factors of mRN
PT preventative research on pathogenic viruses, involves i
PT random oligonucleotide sequences into an untranslated re
XX
PS Example 1; Page 7; 16pp; Japanese.
XX
CC The invention relates to a method of screening potential
CC control factors of mRNA. The method involves synthesizi
CC containing a cap structure and a poly(A) chain sequence
CC random oligonucleotide sequence which is a candidate for
CC control factor is introduced in the 5' untranslated re
CC mRNA in which the translation efficiency is changed com
CC untreated is selected. The method can be used for prov

```
CC   on pathogenic viruses. Sequences ABL41035-42 represent primers used for
CC   amplifying the UTRs of GUS mRNA.
XX
SQ   Sequence 93 BP; 9 A; 12 C; 12 G; 60 T; 0 other;

  Query Match             16.1%;  Score 32.4;  DB 24;  Length 93;
  Best Local Similarity   68.2%;  Pred. No. 2.9e+02;
  Matches   45;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy     128 CGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACA 187
           || |||    || | ||  | | ||  |  ||||||||||||||||||||  || | | |
Db      73 CGCGAACTAAAATCTCGAGCTTCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 14

Qy     188 AACAAA 193
           || |||
Db      13 AAAAAA 8


RESULT 10
AAC78380
ID   AAC78380 standard; cDNA; 89 BP.
XX
AC   AAC78380;
XX
DT   08-FEB 2001  (first entry)
XX
DE   Human cancer associated gene sequence SEQ ID NO:774.
XX
KW   Human; cancer associated gene; cancer antigen; detection; cancer;
KW   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
KW   antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
KW   anti-inflammatory; antithyroid; antiallergic; antibacterial, cardiant;
KW   dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW   vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW   immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW   allergic reaction, graft versus host disease, organ rejection;
KW   haemostatic; thrombolytic; cardiovascular disorder; infection;
KW   neurological disease; drug screening; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055350-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05882.
XX
PR   12-MAR-1999;  99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587533/55.
DR   P-PSDB; AAB44171.
XX
PT   Novel isolated nucleic acids comprising sequences encoding peptides
PT   useful for treating or diagnosing e.g. cancer -
XX
PS   Claim 1; Page 1321; 2352pp; English.
XX
CC   AAC77607 to AAC78448 encode the human cancer associated proteins given
CC   in AAB43998 to AAB44239. The proteins can have activities based on the
CC   tissues and cells the genes are expressed in. Examples of activities
CC   include: cytostatic; proliferative; vulnerary; immunomodulator;
CC   antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
CC   anti-inflammatory; antithyroid; antiallergic; antibacterial, antiviral;
CC   dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC   nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC   polynucleotides and polypeptides can be used for preventing, treating or
CC   ameliorating medical conditions and diagnosing pathological conditions.
CC   Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC   the present invention may be used to treat immune disorders by activating
CC   or inhibiting the proliferation, differentiation or mobilisation of
CC   immune cells, to treat disorders of haematopoietic cells, autoimmune
CC   disorders, allergic reactions, graft versus host disease and organ
CC   rejection, modulate haemostatic or thrombolytic activity, modulate
CC   inflammation, cancers, cardiovascular disorders, neurological disease and
CC   bacterial or viral infections. The peptides, nucleotides, antibodies,
CC   agonists and antagonists may be also be used in drug screens. AAC78449 to
CC   AAC78457 and AAB44240 represent sequences used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 89 BP; 64 A; 4 C; 9 G; 5 T; 7 other;

  Query Match             16.0%;  Score 32.2;  DB 21;  Length 89;
  Best Local Similarity   64.8%;  Pred. No. 4.2e+02;
  Matches   46;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     126 GACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACA 185
           || || || | ||   | | |    ||  |  ||||||||||||||||||||  || | |
Db       5 GAGGGAAACATCAGGNATGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 64

Qy     186 CAAACAAACCA 196
           ||| |||  |
Db      65 AAAAAAAANA 75


RESULT 11
ABK54792/C
ID   ABK54792 standard; cDNA; 74 BP.
XX
AC   ABK54792;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Human colon cancer-associated cDNA, SEQ ID No 262.
XX
KW   Human; colon cancer; immunogenic; vaccine; tumour; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200212280-A2.
XX
PD   14-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US23826.
XX
PR   04-AUG-2000; 2000US-223265P.
PR   02-OCT-2000; 2000US-237406P.
PR   20-MAR-2001; 2001US-277495P.
PR   03-JUL-2001; 2001US-302702P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Pyle RA,  Xu J,  Secrist H;
XX
DR   WPI; 2002-257162/30.
XX
PT   Novel polynucleotide encoding colon tumour polypeptides, useful as
PT   vaccines for treating colon cancers -
XX
PS   Claim 1; Page 225; 425pp; English.
XX
CC   The invention relates to isolated polynucleotides (I) encoding colon
CC   tumour polypeptides (II). (I) is useful for stimulating an immune
CC   response in a patient and treating colon cancer in a patient.
CC   Oligonucleotides derived from (I) are useful for determining the presence
CC   of cancer in a patient. (I) and (II) are useful in pharmaceutical
CC   compositions, e.g. vaccines, and other compositions for the diagnosis
CC   and treatment of colon cancer. A composition comprising a first component
CC   selected from physiologically acceptable carriers and immunostimulants,
CC   and an antigen-presenting cell expressing (II) is useful for inhibiting
CC   development of cancer in a patient. (I) is useful in the design and
CC   preparation of ribozyme molecules for inhibiting expression of tumour
CC   polypeptides and (I). ABK54531-ABK55464 represent human colon cancer cDNA
```

```
CC   Sequences of the invention:
XX
SQ   Sequence 74 BP; 8 A; 7 C; 7 G; 52 T; 0 other;

  Query Match             15.6%;  Score 31.4;  DB 24;  Length 74;
  Best Local Similarity   77.6%;  Pred. No. 6.1e-02;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    4;  Gaps    3;

Qy     145 TTTTTTAATCAGGAAAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
           |||| || | |||||||| |||||||||| || | | ||| | |
Db      66 TTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 18


RESULT 12
AAF22008
ID   AAF22008 standard; DNA; 83 BP.
XX
AC   AAF22008;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Human breast and ovarian cancer associated antigen gene SEQ ID 335.
XX
KW   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW   neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
KW   antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW   Addison's disease; allergy; autoimmune haemolytic anaemia;
KW   autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW   multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW   cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200055173-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05881.
XX
PR   12-MAR-1999;  99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA;  Ruben SM;
XX
DR   WPI; 2000-611515/58.
DR   P-PSDB; AAB59105.
XX
PT   New human breast and ovarian cancer associated gene sequences and the
PT   polypeptides encoded by those genes, useful in the prevention,
PT   treatment and diagnosis of cancer, immune disorders, cardiovascular
PT   disorders and neurological diseases -
XX
PS   Claim 1; Page 825-826; 1299pp; English.
XX
CC   Sequences AAF21614 - AAF22083 represent DNA sequences encoding human
CC   proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC   associated with breast and ovarian cancer. Included in the invention are
CC   sequences AAF22042 - AAF22046 and AAB59129 which are used in the
CC   isolation and characterisation of the DNA and protein sequences of the
CC   invention. The breast and ovarian cancer associated DNA, protein, agonist
CC   or antagonist sequences exhibit cytostatic; immunosuppressive;
CC   neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
CC   antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant;
CC   antibacterial; antifungal; antiparasitic and cardiant activity. The
CC   polynucleotide and protein sequences are used in the diagnosis of cancer,
CC   particularly breast and ovarian cancer. The nucleic acid sequences,
CC   proteins, agonists and agonists may also be used in the diagnosis,
CC   prevention and treatment of immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis, cardiovascular disorders such as
CC   myocardial ischaemias, wound healing, neurological disease
CC   cerebral anoxia and epilepsy; and infectious diseases
XX
SQ   Sequence 83 BP; 72 A; 3 C; 5 G; 2 T; 1 other;

  Query Match             15.6%;  Score 31.4;  DB 21;  Length
  Best Local Similarity   65.7%;  Pred. No. 7.1e-02;
  Matches   44;  Conservative    3;  Mismatches   23;  Indels

Qy     127 AGGGGAAAAACAAACAGTTCCTTAGTAAGACACAAAAAAAAAAAAAAAAAAA
           || | ||||  ||| |          || | ||||||||||||||||||||
Db       9 AGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Qy     187 AAACAAA 193
           ||| |||
Db      69 AAAAAAA 75


RESULT 13
AAQ11764/c
ID   AAQ11764 standard; DNA; 98 BP.
XX
AC   AAQ11764;
XX
DT   22-JUL-1991  (first entry)
XX
DE   Self-complementary, SP6 promoter hairpin-forming sequence
XX
KW   SP6 bacteriophage; DNA-dependent RNA polymerase;
KW   target sequence amplification, ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1..98
FT                   /*tag= a
FT                   /note= "number of 5' & 3' loop is 50"
XX
PN   EP427073-A.
XX
PD   15-MAY-1991.
XX
PF   27-OCT-1990;  90EP-0120650.
XX
PR   28-AUG-1990;  90US-0569991.
PR   09-NOV-1989;  89US-0434372.
XX
PA   (MOLE-) MOLECULAR DIAGNOSTI.
XX
PI   Battaqupta N;
XX
DR   WPI; 1991-141638/20.
XX
PT   Nucleic acid probe for amplification and detection of tar
PT   sequence - capable of forming linear double hairpin structure
PT   promoter and transcribing target sequence, is sensiti
PT   useful in medical diagnosis
XX
PS   Claim 2; Page 11; 15pp; English.
XX
CC   The sequence is an example of a preferred SP6 RNA polyme
CC   promoter for use in the invention. There can be from 1
CC   the loop region. A probe sequence is situated to the 3'
CC   promoter region. Upon hybridisation of the probe to a tar
CC   and ligation of the hybridised target sequence to the 5'
CC   hairpin-forming sequence, the target sequence can be tra
CC   SP6 RNA polymerase. This allows the target sequence to be
CC   (and detected) using a single oligonucleotide component.
CC   See also AAQ11759-Q11763.
XX
SQ   Sequence 98 BP; 15 A; 10 C; 8 G; 55 T; 10 other;

  Query Match             15.6%;  Score 31.4;  DB 12;  Length
```

```
  Best Local Similarity   77.6%;  Pred. No. 6.2e+02;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      151 AATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAACCATTT 199
            ||  |  ||||||||||||||||||  || | | ||||| || ||||
Db       63 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACATACGATTT 15


RESULT 14
AAL29453
ID   AAL29453 standard; DNA; 51 BP.
XX
AC   AAL29453;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #2661.
XX
KW   Immunosuppressive, immunostimulatory, antiinflammatory, cytostatic,
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35498.
XX
PR   28-DEC-1999;  99US-0173419.
PR   27-DEC-2000; 2000US-0173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Loach M;
XX
DR   WPI; 2001-469219/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g.
PT   cancer, autoimmune diseases and infections.
XX
PS   Claim 1; Page 2148; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC   G protein coupled receptors and thioesterases. The present sequence is
CC   one such oligonucleotide. The oligonucleotides and the peptides encoded
CC   by them may be used in the prevention, diagnosis and treatment of
CC   diseases associated with inappropriate expression of the proteins listed
CC   above. Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms.
XX
SQ   Sequence 51 BP; 35 A; 3 C; 4 G; 9 T; 0 other;

  Query Match             15.5%;  Score 31.2;  DB 22;  Length 51;
  Best Local Similarity   81.8%;  Pred. No. 6.6e+02;
  Matches   36;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      138 AAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAA 181
            | | | ||| | |||| ||||||||||||||||||||||  ||
Db        7 ATAAATGTTTCTTAATGAGGAAAAAAAAAAAAAAAAAAAAA 50


RESULT 15
AAL25922/c
ID   AAL25922 standard; cDNA; 84 BP.
XX
AC   AAL25922;
XX
DT   07-DEC-2001  (first entry)
XX
DE   Human breast cancer expressed polynucleotide 18379.
XX
KW   Human; breast cancer; cell marker; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151628 A2.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-US00798.
XX
PR   14-JAN-2000; 2000US-0176077.
PR   14-MAR-2000; 2000US-0189167.
PR   24 MAR 2000; 2000US-0192099
PR   29-MAR-2000; 2000US-0193480.
PR   15 MAY 2000; 2000US-0205230.
PR   09 JUN 2000; 2000US 0211315.
PR   25 JUL 2000; 2000US 0220534.
XX
PA   (MILL ) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2001-451856/48.
XX
PT   New peptide useful as a marker for the diagnosis of breast cancer
XX
PS   Claim 1; Page 3395; 3695pp; English.
XX
CC   The invention relates to human breast cancer expressed polynucleotides
CC   (AAL07544 AAL26789) and methods of assessing whether a patient is
CC   afflicted with breast cancer by examining the correlation between the
CC   expression of certain markers and the cancerous state of breast cells.
CC   The polynucleotides and encoded polypeptides are potential markers for
CC   detecting, diagnosing, monitoring, characterising treating and
CC   potentially preventing breast cancer. The polynucleotides and encoded
CC   polypeptides are also useful for isolating compounds with cytostatic
CC   activity.
XX
SQ   Sequence 84 BP; 3 A; 0 C; 0 G; 81 T; 0 other;

  Query Match             15.5%;  Score 31.2;  DB 22;  Length 84;
  Best Local Similarity   66.2%;  Pred. No. 6.7e+02;
  Matches   45;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      192 AAAACCAAACACGTTCCCTAATCAGCAAAAAAAAAAAAAAAAAAACTAAGACACAAACA 191
            ||||  ||| |        ||  |  ||||||||||||||||||||  || | | ||| |
Db       68 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Qy      192 AACCATTT 199
            ||  ||||
Db        8 AAAAATTT 1


Search completed: May 12, 2003, 00:33:10
Job time : 149 secs
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GenCore version 5.1.4_p5_4573
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M nucleic - nucleic search, using sw model

Run on: May 12, 2003, 00:12:34 ; Search time 955 Seconds
(without alignments)
6125.303 Million cell updates/sec

Title: US-09-917-963-3_COPY_3050_3250
Perfect score: 201
Sequence: 1 ctaaqqqqaaaactaqtattt.....aacacaaaacaaaccaattttt 201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 999600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: qb_ba:*
2: qb_htg:*
3: qb_in:*
4: qb_om:*
5: qb_oz:*
6: qb_pat:*
7: qb_ph:*
8: qb_pl:*
9: qb_pr:*
10: qb_ro:*
11: qb_sts:*
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13: qb_un:*
14: qb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_oz:*
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24: em_ph:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	
1	35.6	17.7	91	3	DDACTIN8A	M2[illegible]
c 2	33.8	16.8	98	6	AX[illegible]	AX[illegible]
c 3	33.6	16.7	77	6	AX[illegible]	AX[illegible]
c 4	33.2	16.5	55	6	AX[illegible]	AX[illegible]
5	33.2	16.5	90	11	G[illegible]	G[illegible]
c 6	33.2	16.5	94	11	G[illegible]	G[illegible]
c 7	33	16.4	75	6	A49118	A4[illegible]
8	32.6	16.2	89	6	AX[illegible]	AX[illegible]
c 9	32.4	16.1	72	6	AX3814[illegible]	AX[illegible]
c 10	32.4	16.1	93	6	AX[illegible]	AX[illegible]
11	32.2	16.0	97	6	AX4821[illegible]	AX[illegible]
c 12	31.4	15.6	74	6	AX381[illegible]	AX[illegible]
c 13	31	15.4	73	6	AX381[illegible]	AX[illegible]
c 14	31	15.4	100	6	AX2697[illegible]	AX[illegible]
15	30.6	15.2	86	6	AX2032[illegible]	AX[illegible]
c 16	30.4	15.1	72	6	AX381[illegible]	AX[illegible]
c 17	30.4	15.1	74	6	AX3814[illegible]	AX[illegible]
c 18	30.4	15.1	81	6	AX3814[illegible]	AX[illegible]
c 19	30.2	15.0	65	6	A62426	A6[illegible]
20	30.2	15.0	77	6	A08908	A[illegible]
21	30.2	15.0	80	6	A[illegible]	A[illegible]
22	30.2	15.0	80	6	AB[illegible]	AB[illegible]
23	30.2	15.0	80	6	AR[illegible]	AR[illegible]
c 24	30.2	15.0	80	6	AB201[illegible]	AB[illegible]
c 25	30.2	15.0	82	6	AX381[illegible]	AX[illegible]
26	30.2	15.0	85	6	AX0994[illegible]	AX[illegible]
c 27	30.2	15.0	90	6	AX2619[illegible]	AX[illegible]
28	30.2	15.0	96	6	A08909	A[illegible]
c 29	30.2	15.0	100	6	AX3814[illegible]	AX[illegible]
c 30	30	14.9	56	6	AX3817[illegible]	AX[illegible]
c 31	30	14.9	76	6	AX381[illegible]	AX[illegible]
c 32	30	14.9	83	6	I46508	I[illegible]
c 33	30	14.9	100	10	BN01[illegible]	
c 34	29.8	14.8	61	6	A62426	A6[illegible]
35	29.8	14.8	62	6	AX20[illegible]	AX[illegible]
36	29.8	14.8	62	9	S52[illegible]	S[illegible]
c 37	29.8	14.8	79	6	AX381[illegible]	AX[illegible]
38	29.6	14.7	71	9	S76[illegible]	S[illegible]
39	29.6	14.7	85	6	B[illegible]	B[illegible]
c 40	29.6	14.7	91	6	AX4664[illegible]	AX[illegible]
c 41	29.6	14.7	93	6	AX1821[illegible]	AX[illegible]
c 42	29.6	14.7	97	6	AX26[illegible]	AX[illegible]
43	29.4	14.6	84	6	AB[illegible]	AB[illegible]
44	29.4	14.6	84	6	AB[illegible]	AB[illegible]
c 45	29.4	14.6	90	6	AR[illegible]	AR[illegible]

ALIGNMENTS

RESULT 1
DDIACTIN8A
LOCUS DDIACTIN8A [illegible] bp DNA [illegible]
DEFINITION Dictyostelium discoideum actin 8 1 gene, 3' [illegible].
ACCESSION M25215
VERSION M25215.1 GI:1066510
KEYWORDS actin.
SOURCE Dictyostelium discoideum DNA.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelidae; Dictyoste[illegible]
REFERENCE 1 (bases 1 to 91)
AUTHORS McKeown,M., Hirth,K.L., Edwards,S. and Firtel,R.
TITLE Examination of the regulation of the actin [illegible]
Dictyostelium discoideum
JOURNAL Prog. Clin. Biol. Res. [illegible] A 51 7[illegible] (198[illegible])

```
  MEDLINE   82275208
   PUBMED   7051026
COMMENT     On Nov 21, 1995 this sequence version replaced gi:341298.
FEATURES             Location/Qualifiers
     source          1..91
                     /organism="Dictyostelium discoideum"
                     /db_xref="taxon:44689"
BASE COUNT       30 a       2 c       2 g      17 t
ORIGIN

  Query Match             17.7%;  Score 35.6;  DB 3;  Length 91;
  Best Local Similarity   64.6%;  Pred. No. 9.2e-02;
  Matches   53;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy     112 ACTTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAA 171
           | ||  |||| | |   |||| |||| |    |||||  ||||||||||||||
Db       3 AATTATTTAATAAATAATAAAAAAACAAATTGTTGTAATAATCTAAAAAAAAAAAAAAA 62

Qy     172 AAAAAAGTAAGACACAAACAAA 193
           |||||| || | | ||| |||
Db      63 AAAAAAAAAAAAAAAAAAAAA 84


RESULT 2
AX320854/c
LOCUS       AX320854                  98 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 24 from Patent WO0183736.
ACCESSION   AX320854
VERSION     AX320854.1  GI:17902405
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1
  AUTHORS   Pelletier,C. and Kukolj,G.
  TITLE     Internal de novo initiation sites of the hcv ns5b polymerase and
            use thereof
  JOURNAL   Patent: WO 0183736-A 24 08-NOV-2001;
            BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES             Location/Qualifiers
     source          1..98
                     /organism="Hepatitis C virus"
                     /db_xref="taxon:11103"
BASE COUNT       24 a       5 c       1 g      90 t
ORIGIN

  Query Match             16.8%;  Score 33.8;  DB 6;  Length 98;
  Best Local Similarity   62.4%;  Pred. No. 2.1e+03;
  Matches   53;  Conservative    5;  Mismatches   32;  Indels    0;  Gaps    0;

Qy     109 AGGACTTCCTTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAA 168
           ||| |     || | | ||||||  ||| |        || | ||||||||||
Db      95 AGCAATATAAAAAAAAAAAAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 37

Qy     169 AAAAAAAAGTAAGACACAAACAAA 193
           |||||||||  || | | |||||||
Db      36 AAAAAAAAAAAAAAAAAAAACAAA 11


RESULT 3
AX256011/c
LOCUS       AX256011                  77 bp    DNA     linear   PAT 16-OCT-2001
DEFINITION  Sequence 162 from Patent WO0170976.
ACCESSION   AX256011
VERSION     AX256011.1  GI:16075051
KEYWORDS
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Xu,J., Pyle,R.A. and Stolk,J.A.
  TITLE     Compositions and methods for the therapy and diagnosis of ovarian
            and endometrial cancer
  JOURNAL   Patent: WO 0170976 A 162 27-SEP-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..77
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       9 a       5 c       7 g      53 t       3 others
ORIGIN

  Query Match             16.7%;  Score 33.6;  DB 6;  Length 77;
  Best Local Similarity   64.0%;  Pred. No. 2.4e+03;
  Matches   48;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy     118 TTAAGCATGACGGGAAAACCAAACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAA 177
           | ||  || |  |||| | |     |||||||| |  |||||||||||||  |||||
Db      77 TCAAAAATAAAAGCAACCCAGATTTNTTCCCTAAAAAAAAAAAAAAAAAAAANNAAAAA 18

Qy     178 GTAAGACACAAACAA 192
           || | | ||| ||
Db      17 AAAAAAAAAAAAAA 3


RESULT 4
AX396936/c
LOCUS       AX396936                  55 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 1151 from Patent WO0212328.
ACCESSION   AX396936
VERSION     AX396936.1  GI:21067683
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
  TITLE     Compositions and methods for the therapy and diagnosis of colon
            cancer
  JOURNAL   Patent: WO 0212328 A 1151 14-FEB-2002;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..55
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       6 a       2 c       6 g      41 t
ORIGIN

  Query Match             16.5%;  Score 33.2;  DB 6;  Length 55;
  Best Local Similarity   75.9%;  Pred. No. 3e+03;
  Matches   41;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     140 ACACGTTCCCTAATCAGGAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 193
           | || |||||  | ||  | ||||||||||||||||||  || | | ||| |||
Db      55 AAACCTTCCCAATTCTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 5
G37815
LOCUS       G37815                    90 bp    DNA     linear   STS 24-MAR-1999
DEFINITION  ACT1 Plasmodium falciparum haploid Plasmodium falciparum STS
            genomic, sequence tagged site.
ACCESSION   G37815
VERSION     G37815.1  GI:3815421
KEYWORDS    STS.
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Su,X.-z., Ferdig,M.T. and Wellems,T.E.
  TITLE     Integrated genetic and physical maps of Plasmodium falciparum
  JOURNAL   Unpublished (1998)
COMMENT     Synonyms: ACT1
```

Author: Thomas E. Wellems
LMI
NIAID
Bldg. 4, Room 126, NIH Campus, Bethesda, MD 20892-0425
Tel: (301) 496-4621
Fax: (301) 402-0078
Email: tew@helix.nih.gov
Primer A: ACAGAACTATATACAAC
Primer B: AICTTICTTICTAIGCG
SIS size: 90
PCR Profile:
Initial heat: 2min at 94oC
Cycles: 40 cycles, each having steps 1 sec at 94oC; 1sec at 45oC; 1sec at 40oC; 1sec at 72oC
Machine: Perkin Elmer GeneAmp 9600
Protocol:
Template: 1-10 ng
Primer: 5 pM each
dNTPs: 0.8 ml of 10 mM stock solution
Taq Polymerase: 0.5 unit
Total Volume: 25 ul

Buffer:
10 mM Tris-HCl, pH 8.3
1.5 mM MgCl2
50 mM KCl.

FEATURES Location/Qualifiers
source 1..90
/organism="Plasmodium falciparum"
/strain="HB3clz"
/db_xref="taxon:5833"
/map="6"
/clone_lib="Plasmodium falciparum...gt11"
/dev_stage="erythrocytic hepatic stage"
SIS 1..90
primer_bind 1..18
primer_bind complement(73..90)
BASE COUNT 67 a 10 c 8 g 5 t
ORIGIN

Query Match 16.5%; Score 63.2; DB 11; Length 90;
Best Local Similarity 71.0%; Pred. No. 2.8e-03;
Matches 44; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

Qy 132 AAAACAAACACGTTCCTAACACGAAAAAAAAAAAAAAAAAAAA 175
|| | || | | | | | | ||||||||||||||||||||
Db 3 AGAACTATATACATACTCAAAAAAAAAAAAAAAAAAAAAAAAAA 46

Qy 192 AA 193
||
Db 24 AA 24

RESULT 6
X73641/c
LOCUS X73641 94 bp DNA linear SIS 15-JUL-2002
DEFINITION BZ096F chloated leaf tissue of rice Oryza sativa SIS genomic clone
BZ096 sequencing direction forward, sequence tagged site.
ACCESSION X73641
VERSION X73641.1 GI:19072
KEYWORDS SIS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 94)
AUTHORS McCouch,S.R.
TITLE Oryza sativa SIS
JOURNAL Unpublished (2002)
COMMENT
Contact: Susan R. McCouch
Cornell University
Dept. of Plant Breeding
Ithaca, NY 14853-1901
Tel: 6072550420
Fax: 6072556683
Email: srm4@cornell.edu
Primer A: M13 universal forward (TAAAACGACGGCCAG)
Primer B: M13 Universal Reverse (AACAGCTATGACCATG)
SIS size: 94
Protocol:
Template: 20-100 ng
Primer: 5pmol each
dNTPs: 40nmol
Taq polymerase: 5 units
Total volume: 50 ul

Buffer:
Tris-HCl: 100mM
KCl: 500mM
MgCl2: 15mM
Gelatin: 0.1%
PH: 8.3

This is a partial sequence of the RFLP probe that was
mapped at Cornell University's Plant Breeding Dept.
the Genome Sequencing Center at Cold Spring Harbo
marker is located on rice chromosome 3. For
related information, see www.gramene.org/rflp/probes.html
Gramene database at http://www.gramene.org.

FEATURES Location/Qualifiers
source 1..94
/organism="Oryza sativa"
/cultivar="IR66"
/db_xref="taxon:4530"
/map="3"
/clone="BZ096F"
/clone_lib="Total leaf tissue of rice
/note="Vector: lambda ZAP II/pBluescript
A Lambda ZAP II cDNA library was constr
extracted from chloated leaf tissue of
'IR66' and converted to pBluescript (Stra
described in Krause et al. (1994) Genet.
For insert amplification, use M13 forward
primers. Restriction site is EcoRI. The
library are dephosphorylated with the prot
SIS 1..94
BASE COUNT 2 a 6 c 12 g 74 t
ORIGIN

Query Match 16.5%; Score 63.2; DB 11; Length
Best Local Similarity 71.0%; Pred. No. 2.8e-03;
Matches 44; Conservative 0; Mismatches 18; Indels 1;

Qy 132 AAAACAAACACGTTCCTAACACGAAAAAAAAAAAAAAAAAAAA 175
|| | || | | | | | | ||||||||||||||||||||
Db 24 AGAACTATATACATACTCAAAAAAAAAAAAAAAAAAAAAAAAAA 67

Qy 192 AA 193
||
Db 24 AA 23

RESULT 7
A49118/c
LOCUS A49118 19 DNA linear
DEFINITION Sequence 19 from Patent WO 9...
ACCESSION A49118
VERSION A49118.1 GI:2652674
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Mitochondrion Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
REFERENCE 1 (bases 1 to 19)
AUTHORS Jolly,C. and Sullivan,K.

```
  TITLE     NUCLEOTIDE SEQUENCING METHOD
  JOURNAL   Patent: WO 9606187-A 13 29-FEB-1996;
            SOLICITOR FOR THE AFFAIRS OF H (GB)
COMMENT     Other publication AU 6264095 960314.
FEATURES             Location/Qualifiers
     source          1..75
                     /organism "Homo sapiens"
                     /organelle "mitochondrion"
                     /db_xref="taxon:9606"
BASE COUNT         5 a       4 c      11 g      54 t       1 others
ORIGIN

  Query Match             16.4%;  Score 34;  DB 6;  Length 75;
  Best Local Similarity   74.7%;  Pred. No. 4.2e-03;
  Matches   42;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     137 AAAACAGGTTCCCIAATCAGGAAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAAA 194
           ||| || || |   ||||   |||||||||||||||||||  || | | ||| ||
Db      64 CAAGCAAGTACAGCAATCAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 8
AX203299
LOCUS       AX203299                  89 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 44 from Patent WO0154836.
ACCESSION   AX203299
VERSION     AX203299.1  GI:15392669
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 89)
  AUTHORS   Schlegel,R., Endege,W. and Monahan,J.E.
  TITLE     Identification, assessment, prevention, and therapy of prostate
            cancer
  JOURNAL   Patent: WO 0154836-A 44 26-JUL-2001;
            Millennium Predictive Medicine, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..89
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        66 a       4 c       9 g      11 t
ORIGIN

  Query Match             16.2%;  Score 32.6;  DB 6;  Length 89;
  Best Local Similarity   64.3%;  Pred. No. 3.8e-03;
  Matches   50;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy     111 CAT[illegible]AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 170
           | ||  |||||   | |||  |||  |||  |          || |  ||  ||| | |||
Db      11 GAATTAATTAAGGCGGTCGGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 70

Qy     171 AAAAAAAGTAAGACACAAA 189
           ||||||  || | | |||
Db      71 AAAAAAAAAAAAAAAAAA 89


RESULT 9
AX381405/c
LOCUS       AX381405                  72 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 343 from Patent WO0212280.
ACCESSION   AX381405
VERSION     AX381405.1  GI:19576224
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lyle,R.A., Xu,J. and Seerist,B.
  TITLE     Compositions and methods for the therapy and diagnosis of colon
            cancer
  JOURNAL   Patent: WO 0212280 A 343 14-FEB-2002;
            GORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..72
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
BASE COUNT         4 a       7 c       7 g      51 t       3 others
ORIGIN

  Query Match             16.1%;  Score 32.4;  DB 6;  Length 72;
  Best Local Similarity   68.9%;  Pred. No. 4.3e+03;
  Matches   42;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy     133 AAACCAAACACCTTCCCIAATCAGGAAAAAAAAAAAAAAAAAAAAGTAAGACACAAACAA 192
           ||| ||    |  ||| ||  |  ||||||||||||||||||||  || | | ||| ||
Db      70 AAANAAATTTGGNNCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 11

Qy     193 A 193
           |
Db      10 A 10


RESULT 10
AX420853/c
LOCUS       AX420853                  93 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 23 from Patent WO0183736.
ACCESSION   AX420853
VERSION     AX420853.1  GI:17902404
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1
  AUTHORS   Pellerin,C. and Rakolj,G.
  TITLE     Internal de novo initiation sites of the hcv ns5B polymerase and
            use thereof
  JOURNAL   Patent: WO 0183736-A 23 08-NOV-2001;
            BOEHRINGER INGELHEIM (CANADA) Ltd. (CA)
FEATURES             Location/Qualifiers
     source          1..93
                     /organism "Hepatitis C virus"
                     /db_xref "taxon:11103"
BASE COUNT         2 a       7 c       2 g      82 t
ORIGIN

  Query Match             16.1%;  Score 32.4;  DB 6;  Length 93;
  Best Local Similarity   64.9%;  Pred. No. 4.1e+03;
  Matches   48;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy     120 AAGCATGACGGGAAAACCAAACACGTTCCCIAATCAGGAAAAAAAAAAAAAAAAAAAGT 179
           ||| |  | || ||||  ||| |          || |  |||||||||||||||||||
Db      74 AAGGAAAAACGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGC 15

Qy     180 AAGACACAAACAAA 193
           || | | | | |||
Db      14 AAAAAAAAAAAAA 1


RESULT 11
AX482104
LOCUS       AX482104                  97 bp    DNA     linear   PAT 15-AUG-2002
DEFINITION  Sequence 81 from Patent EP1225233.
ACCESSION   AX482104
VERSION     AX482104.1  GI:22316826
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van der Kuyl,A.C. and Cornelissen,M.
  TITLE     Means and methods for treatment evaluation
  JOURNAL   Patent: EP 1225233-A 81 24-JUL-2002;
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            Amsterdam Support Diagnostics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1..97
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="IA0342 (StabAthesin, also called Stab 2) in plasmid
                     number XM_016245)"
BASE COUNT        41 a      26 c      14 g      17 t
ORIGIN

  Query Match             10.4%;  Score 42.2;  DB 6;  Length 97;
  Best Local Similarity   84.6%;  Pred. No. 4.5e+03;
  Matches   44;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy      1 TCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 97
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28 TCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 77

Qy     98 AAAAAAAAAAAAAAAAA 122
          |||||||||||||||||
Db     78 AAAAAAAAAAAAAAAAA 94


RESULT 12
AX981424/c
LOCUS       AX981424                  74 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 262 from Patent WO0212280.
ACCESSION   AX981424
VERSION     AX981424.1  GI:19576243
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Pyle,R.A., Xu,J. and Seerist,H.
  TITLE     Compositions and methods for the therapy and diagnosis of ovarian
            cancer
  JOURNAL   Patent: WO 0212280-A 262 14-FEB 2002;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..74
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        8 a       7 c       7 g      52 t
ORIGIN

  Query Match             10.4%;  Score 42.2;  DB 6;  Length 74;
  Best Local Similarity   77.6%;  Pred. No. 4.5e+03;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    3;  Gaps    0;

Qy     14 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 13
AX981604/c
LOCUS       AX981604                  73 bp    DNA     linear   PAT 19-MAR-2002
DEFINITION  Sequence 542 from Patent WO0212280.
ACCESSION   AX981604
VERSION     AX981604.1  GI:19576429
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Pyle,R.A., Xu,J. and Seerist,H.
  TITLE     Compositions and methods for the therapy and diagnosis of ovarian
            cancer
  JOURNAL   Patent: WO 0212280-A 542 14-FEB 2002;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..73
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        8 a       7 c       7 g      51 t
ORIGIN

  Query Match             10.4%;  Score 42.2;  DB 6;  Length 73;
  Best Local Similarity   77.6%;  Pred. No. 4.5e+03;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    3;  Gaps    0;

Qy     14 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


FEATURES             Location/Qualifiers
     source          1..73
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        8 a       7 c       7 g      51 t
ORIGIN

  Query Match             10.4%;  Score 42.2;  DB 6;  Length 73;
  Best Local Similarity   77.6%;  Pred. No. 4.5e+03;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    3;  Gaps    0;

Qy     14 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 TTCCCCTAATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 14
AX266734/c
LOCUS       AX266734                  [illegible] bp    DNA     linear   PAT
DEFINITION  Sequence 385 from Patent W[illegible].
ACCESSION   AX266734
VERSION     AX266734.1  GI:16502[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Meagher,M.J., Xu,J. and Kinn,S.L.
  TITLE     Compositions and methods for the therapy and diagnosis of [illegible]
  JOURNAL   Patent: WO 0173027 A [illegible] [illegible]
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1..100
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        5 a       5 c       [illegible] g      [illegible] t
ORIGIN

  Query Match             10.4%;  Score 42.2;  DB 6;  Length [illegible];
  Best Local Similarity   62.2%;  Pred. No. [illegible]e+03;
  Matches   46;  Conservative    0;  Mismatches   28;  Indels    [illegible];

Qy     14 AATTACTAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 193
          |  ||| | |  ||||  |||| |           | | ||||||||||||
Db     80 ANANATAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 131

Qy    194 AACTACAAACAAA 193
          ||| | | |||| |||
Db     26 AAAAAAAAAAAAA 13


RESULT 15
AX203294
LOCUS       AX203294                  [illegible] bp    DNA     linear   PAT
DEFINITION  Sequence 39 from Patent W[illegible].
ACCESSION   AX203294
VERSION     AX203294.1  GI:1549[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Schlegel,K., Endege,W. and M[illegible].
  TITLE     Identification, assessment [illegible] and therap
            cancer
  JOURNAL   Patent: WO 0[illegible]3846 A [illegible] [illegible]
            Millennium Predictive Medicine [illegible] (US)
FEATURES             Location/Qualifiers
     source          1..86
                     /organism="H[illegible] sapiens"
                     /db_xref="taxon:[illegible]"
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BASE COUNT 65 a 5 c 3 g 12 t 1 others
ORIGIN

Query Match 15.2%; Score 40.6; DB 6; Length 86;
Best Local Similarity 68.9%; Pred. No. 9.6e+03;
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 133 AAACCAAACAAGTTCCTTAATCAGGAAAAAAAAAAAAAAAAAAAACTAACACACAAACAA 192
||| || ||| | || | ||||||||||||||||||| || | | ||| ||
Db 20 AAAACAGACAATTCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 79

Qy 193 A 193
|
Db 80 A 80

Search completed: May 12, 2003, 00:49:22
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